

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2004, 16:54:34 ; Search time 4445 Seconds
(without alignments)

2905.787 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543

Sequence: 1 MTEQAISFAKDFLAGGIAAA.....LRNGGAFVLVLYDELKKVI 298

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1543	100.0	897	6	BD249697	BD249697 Productio
2	1543	100.0	897	6	AR316657	AR316657 Sequence
3	1543	100.0	897	6	AX134720	AX134720 Sequence
4	1543	100.0	897	6	AX301848	AX301848 Sequence
5	1543	100.0	1184	9	BC008935	BC008935 Homo sapi
6	1543	100.0	1212	6	AR339196	AR339196 Sequence
7	1543	100.0	1308	9	BC007295	BC007295 Homo sapi
8	1543	100.0	1344	9	AY007135	AY007135 Homo sapi
9	1543	100.0	1357	9	BC007850	BC007850 Homo sapi
10	1543	100.0	1399	9	BC031912	BC031912 Homo sapi
11	1543	100.0	1457	9	BC008737	BC008737 Homo sapi
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16	1454	94.2	897	6	BD249696	BD249696 Productio
17	1454	94.2	897	6	AR316656	AR316656 Sequence
18	1454	94.2	897	6	AX134719	AX134719 Sequence
19	1454	94.2	897	6	AX301847	AX301847 Sequence
20	1454	94.2	1228	6	AX771588	AX771588 Sequence
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27	1446	93.7	1297	5	AY398420	AY398420 Danio rer
28	1445	93.6	897	10	MMU10404	U10404 Mus musculu
29	1445	93.6	1236	10	BC004570	BC004570 Mus musculu
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31	1445	93.6	1280	10	MMANTAP	X70847 M.musculus
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39	1421	92.1	1329	5	BC059739	BC059739 Silurana
40	1418	91.9	1070	10	BC026925	BC026925 Mus muscu
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45	1409	91.3	1310	9	BC063643	BC063643 Homo sapi

ALIGNMENTS

RESULT 1

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LOCUS      BD249697      897 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Production of adenine nucleotide translocator (ANT), novel ANT
            ligand, and screening assay thereof.
ACCESSION  BD249697
VERSION    BD249697.1 GI:33059467
KEYWORDS   JP 2002539761-A/3.
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 897)
AUTHORS   Anderson,C.M., Davis,R.E., Clevenger,W., Wiley,S.E., Miller,S.W.,
            Szabo,R.K. and Ghosh,S.S.
TITLE     Production of adenine nucleotide translocator (ANT), novel ANT
            ligand, and screening assay thereof
JOURNAL    Patent: JP 2002539761-A 3 26-NOV-2002;
            MITOKOR
COMMENT    OS Homo sapiens (human)
            PN JP 2002539761-A/3
            PD 26-NOV-2002
            PR 03-NOV-1999 JP 2000579742
            PR 03-NOV-1998 US 09/185904,08-SEP-1999 US 09/393441 PI
            CHRISTEN M ANDERSON,ROBERT E DAVIS,WILLIAM CLEVENGER,SANDRA PI
            EILEEN WILEY.
            PI SCOTT W MILLER,TOMAS R SZABO,SOUNMITRA S GHOSH PC
            C12N15/09,A61K31/704,A61K31/7048,A61K31/7056,A61K31/7064, PC
            A61K45/00,
            PC A61P3/00,A61P3/10,A61P17/06,A61P25/09,A61P25/14,A61P25/16, PC
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            C12P21/02,C12Q1/02,
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            CC screening assay thereof
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Pred. No.: 1,03e-144 Length: 897
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
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101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
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121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
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261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
781 ATCTTCAGAGATGAGGGGGCAAGGCTTCTTCAAGGTCGCTGTCCTCAACGCTCCTCGCG 840
281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
841 GGCATGGGGGCGGCTTCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 894

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LOCUS      AR316657
DEFINITION Sequence 3 from patent US 6562563.
ACCESSION  AR316657
VERSION    AR316657.1 GI:33695603
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 897)
AUTHORS   Murphy,A.N., Clevenger,W., Wiley,S.E., Andreyev,A.Y., Frigeri,L.G.,
            Velecelebi,G. and Davis,R.E.
TITLE     Compositions and methods for determining interactions of
            mitochondrial components, and for identifying agents that alter
            such interactions
JOURNAL    Patent: US 6562563-A 3 13-MAY-2003;
FEATURES   Location/Qualifiers
            source 1..897
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ORIGIN
Alignment Scores:
Pred. No.: 1,03e-144 Length: 897
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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RESULT 3
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DEFINITION
Sequence 3 from Patent WO0132876.
AX134720
ACCESSION
AX134720.1 GI:14271237
VERSION
KEYWORDS

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Murphy, A.N., Clevenger, W., Wiley, S.E., Andreyev, A.Y., Frigeri, L.G., Velicelbi, G. and Davis, R.E.
Compositions and methods for determining interactions of mitochondrial components, and for identifying agents that alter such interactions
Patent: WO 0132876-A 3 10-MAY-2001;
MITOKOR (US)

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Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 1.03e-144 Length: 897
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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 DEFINITION Sequence 3 from Patent WO0185944.
 ACCESSION AX301848
 VERSION AX301848.1 GI:17382905
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 Anderson, C.M., Davis, R.E., Clevenger, W., Wiley, S.E., Miller, S.W., Szabo, T.R., Ghosh, S.S., Mocs, W.H., Pei, Y., and Carroll, A.K.
 Production of adenine nucleotide translocator (ant), novel ant
 ligands and screening assays therefor
 Patent: WO 0185944-A 3 15-NOV-2001;
 JOURNAL MITOKOR (US)

FEATURES
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ORIGIN
 Alignment Scores:
 Pred. No.: 1.03e-144 Length: 897
 Score: 1543.00 Matches: 298
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-811-094-33 (1-298) x AX301848 (1-897)

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 QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
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 Db 841 GGCATGGGGGGCGCTCTGCTGCTGTGTACGAGGCTCAAGAAGGTGATC 894

RESULT 5
 BC008935
 LOCUS
 DEFINITION Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6, mRNA (cDNA clone MGC:2387 IMAGE:2824067), complete cds.
 ACCESSION BC008935
 VERSION BC008935.2 GI:33874058
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 1184)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Warra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE	22388257	1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
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AUTHORS	Strausberg,R.	
TITLE	Direct Submission	
JOURNAL	Submitted (29-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC) Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT	On Aug 19, 2003 this sequence version replaced gi:14286273. Contact: MGC help desk Email: cgabbs-r@mail.nih.gov Tissue Procurement: DCTD/PTP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: the I.M.A.G.E. Consortium (LILNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbio.org contact: amadansystemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting	
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QY	41	AlaSerLysGlnIleAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 60
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QY	61	IleProLysGluGlnGlyValLeuSerPheThrPheArgGlyValAsnLeuAlaAsnValIleArg 80
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QY	81	TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
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QY	101	GlyGlyValAspLysHisThrGlnPheThrPheArgTyrPheAlaGlyValAsnLeuAlaSerGly 120
Db	385	GGGGGGCTGGACNAGCACAGCAGTCTTGAGGTACTTTGCGGGCACTTGCGCTCCGGC 444
QY	121	GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
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QY	141	LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
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Db	745	ACGGCGTGGCGCGTGTGTCTTACCTTCCACACGCGTGGCGGCGCGCATGATGATG 804
QY	241	GlnSerGlyArgLysGlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 260
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DEFINITION	Sequence 687 from patent US 6589662.	
ACCESSION	AR339196	
VERSION	AR339196.1	GI:33726053
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 1212)	
AUTHORS	Tang,Y.T., Zhou,P. and Drmanac,R.T.	
TITLE	Nucleic acids and polypeptides	

JOURNAL Patent: US 659662-A 687 27-MAY-2003;
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Alignment Scores:

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 Score: 1543.00 Matches: 298
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US-09-811-094-33 (1-298) x AR339196 (1-1212)

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 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
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LOCUS

DEFINITION

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adenine nucleotide translocator), member 6, mRNA (cDNA clone

MGC:15671 IMAGE:3349670), complete cds.

BC007295

BC007295.1 GI:13938330

MGC.

Homo sapiens

Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

1. (bases 1 to 1308)

Strausberg,R.D., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullahy,S.J., Bosak,S.A., McSwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahney,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Boutard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E.,

Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2. (bases 1 to 1308)

Strausberg,R.

Direct Submission

Submitted (01-MAY-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Varon Butterfield,

Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin,

Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candace McLeavy, Steven

Nees, Pawan Pandoh, Anna-Lilisa Prabhu, Parvaneh Saeedi, Jacqueline

Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott,

Michael Thorne, Mitranada Tsai, Natasja van den Bosch, Jill Vardy,

George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>

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Location/Qualifiers

1. 1308

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AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	Andersson, B., Wentland, M.A., Ricafrente, J.Y., Liu, W. and Gibbs, R.A.			
JOURNAL	A 'double adaptor' method for improved shotgun library construction			
MEDLINE	Anal. Biochem. 236 (1), 107-113 (1996)			
PUBMED	96207227			
REFERENCE				
AUTHORS	2 (bases 1 to 1344)			
TITLE	Yu, W., Andersson, B., Worley, K.C., Muzny, D.M., Ding, Y., Liu, W., Ricafrente, J.Y., Wentland, M.A., Lennon, G. and Gibbs, R.A.			
JOURNAL	Large-scale concatenation cDNA sequencing			
MEDLINE	Genome Res. 7 (4), 353-358 (1997)			
PUBMED	97264341			
REFERENCE				
AUTHORS	3 (bases 1 to 1344)			
TITLE	Zhou, J., Yu, W., Tang, H., Mei, G., Tsang, Y.T.M., Bouck, J., Gibbs, R.A.			
JOURNAL	Direct Submission			
MEDLINE	Submitted (24-JUL-2000) Human Genome Sequencing Center and Texas Children's Cancer Center, Baylor College of Medicine, Houston, TX			
PUBMED	77030, USA			
COMMENT	The clone request should be directed to Dr. J. Margolin at Pediatrics-Hematology & Oncology, Texas Children's PEIGIN Center 102514, Houston, Texas 77030, USA. Telephone: 713-770-4583			
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Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: JRAL Plate: 20 Row: i Column: 14.

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source

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gene

CDS

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misc_feature

ORIGIN

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Query Match: 100.00% Indels: 0
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US-09-811-094-33 (1-298) x BC007850 (1-1357)

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Db 812 CAGTCCGGCGCAAGGAGCTGACATCATGTACACGGGCGCGTGCATCTTGGAGGAG 871
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LOCUS BC031912 1399 bp mRNA linear PRI 12-NOV-2003
DEFINITION Homo sapiens soluble carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6, mRNA (cDNA clone MGC:29984 IMAGE:5141625), complete cds.
ACCESSION BC031912
VERSION BC031912.1 GI:21594692
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1399)
AUTHORS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Young A.C., Shchepochko Y., Sanchez A., Whitting M., Madan A., Young A.C., Green E.D., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywicki M.I., Skalska U., Marra M.A., Schneringer A., Schein J.E., Jones S.J. and Marra M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22398257

12477932
PUBMED
REFERENCE
2 (bases 1 to 1399)
Strausberg, R.
AUTHORS
TITLE
Direct Submission
JOURNAL
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounsgood, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 42 Row: P Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.

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Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x BC031912 (1-1399)

BC008737 1457 bp mRNA linear PRI 04-OCT-2003
Homo sapiens solute carrier family 25 (mitochondrial carrier;
adenine nucleotide translocator), member 6, mRNA (cDNA clone
MGC:3042 IMAGE:3342722), complete cds.

BC008737
Accession
BC008737.2 GI:33873986
Version
MGC.
Keywords
Homo sapiens (human)
Source
Homo sapiens
Organism
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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98 ATCTCCAAAGACGGCGGTGCTCCATCAGCGGGTCAAGCTGCTGCTGAGGTCCAGCAC 157
41 AlaSerIysGlnIleAlaAlaAspLysGlnIysGlyIleValAlaAspCysIleValArg 60
158 GCCAGCAGCAGATCGCGCGCGACAGCAGTACAGGGCATCGTGACTGCATTGTCCGC 217
61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
218 ATCCCAAGGACGAGCGGTGCTCTCTCTGAGGGGCAACCTTGCCAACTCATTTCCG 277
81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
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121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaAspThrArg 140
398 GTGTGGCGCGCGCGACCTCCCTCTGCTTGTGTACCGCTGGATTTTGCAGAACCCGC 457
141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
458 CTGGCAGCGGACGTGGGAAAGTCAAGCACAGGCGCGAGTTCGAGGCTTGGGAGACTGC 517
161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
518 CTGTGTAAGATCACCAAGTCCGACGGCATCGGGGCTGTACCAAGGCTTCAGTGTCTCC 577
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638 ATGTCCTCCCGACCCCAAGAACACGACATCATGTGTGTGAGCTGGATGATCGCGACCG 697
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758 CAGTCGGGGCCAAAGAGAGTGCATCATGTATACAGGGCACCGTCGACTGTGTGGAGAA 817
261 IlePheArgAspGluGlyGlyValAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
818 ATCTTCAGAGATAGGGGGGCAAGCCCTTCTCAAGGGTGGTGTCTCAACGTCCTCGCG 877
281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
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BC008737
LOCUS
DEFINITION
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adenine nucleotide translocator), member 6, mRNA (cDNA clone
MGC:3042 IMAGE:3342722), complete cds.

ACCESSION
BC008737
VERSION
BC008737.2
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1457)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Nath,K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Narusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,W.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Faney,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,
Schnier,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)
22388257
12477932
2 (bases 1 to 1457)
Strausberg,R
Direct Submission
Submitted (25-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:14250566.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Contact: nisc.mgc@nhgri.nih.gov
Web site: http://www.nisc.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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Young,A., Zhang,L.-H. and Green,E.D.
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through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
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Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
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RESULT 13

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DEFINITION Bovine ADP/ATP translocase T2 mRNA, complete cds.
ACCESSION M24103 J02845
VERSION M24103.1 GI:529416
KEYWORDS ADP/ATP translocase; translocase.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 1349)
AUTHORS Powell, S.J., Mead, S.M., Runswick, M.J. and Walker, J.E.
TITLE Two bovine genes for mitochondrial ADP/ATP translocase expressed
differences in various tissues
JOURNAL Biochemistry 28 (2), 866-873 (1989)
MEDLINE 89229093
PUBMED 2540808
COMMENT On Aug 13, 1994 this sequence version replaced gi:341114.
Original source text: Bos taurus cDNA to mRNA.
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US-09-811-094-33 (1-298) x BOVT2TRANS (1-1349)

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DEFINITION   Gallus gallus avant mRNA for ATP/ADP antiporter, complete cds.
ACCESSION   AB088686
VERSION     AB088686.1   GI:22775581
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ORGANISM    Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE   1
AUTHORS    Toyomizu,M., Ueda,S., Sato,S., Seki,Y., Sato,K. and Akiba,Y.
TITLE      Cold-induced mitochondrial uncoupling and expression of chicken UCP
           and ANT mRNA in chicken skeletal muscle
JOURNAL    FEBS Lett. (2002) in press
AUTHORS    Ueda,M., Seki,Y., Sato,S., Akiba,Y. and Toyomizu,M.
TITLE      Direct Submission
JOURNAL    Submitted (24-JUL-2002) Masaaki Toyomizu, Tohoku University, Life
           Science, Graduate School of Agriculture, 1-1
           Tsutsumidori-Amamiyamachi, Sendai, Miyagi 981-8555, Japan
           (E-mail:toyomizu@bios.tohoku.ac.jp,
           URL:http://www.bios.tohoku.ac.jp/animutr/, Tel:81-22-717-8690,
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LOCUS   BC056160                1251 bp    mRNA    linear    PRI 08-OCT-2003
DEFINITION   Homo sapiens solute carrier family 25 (mitochondrial carrier;
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ACCESSION   BC056160
VERSION     BC056160.1   GI:33525217
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1251)
AUTHORS    Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
           Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
           Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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           Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

```

Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, X.S., Krzyzanski, M.I., Skalska, J., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin, Leticia Hsiao, Martin Krzyzanski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Nees, Pawan Pandoh, Anna-Jiisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smallos, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAP Plate: 119 Row: a Column: 7
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502098.

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 Query Match: 94.82%
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REMARK
 COMMENT

Wed Aug 18 16:42:48 2004

us-09-811-094-33.rge

Page 16

Search completed: August 17, 2004, 19:25:45
Job time : 4461 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2004, 16:56:19 ; Search time 473 Seconds
(without alignments)

2676.455 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543

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Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1543	100.0	2035	4	AAI60583 Human pol
7	1510	97.9	2592	7	ABX63152 Human cdn
8	1463	94.8	1225	6	AAI46635 Human ins

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13	1424	92.3	1196	9	ADB57820	Adb57820 Toxicity-
14	1424	92.3	1196	9	ADB52341	Adb52341 Primary r
15	1418	91.9	2213	7	ACC46652	Acc46652 Human dit
16	1417	91.8	1156	5	AAS91243	Aas91243 DNA encod
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18	1405	91.1	1259	2	AAV36480	Aav36480 Ant1 cdna
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20	1385	89.8	894	4	AAS05901	Aas05901 Human ade
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22	1385	89.8	1024	7	ABZ83302	Abz83302 Toxicolog
23	1385	89.8	1320	6	ABSE6029	Abse6029 Invertebr
24	1356	87.9	1116	6	ABL69347	AbL69347 Prostate
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27	1289	83.5	552	9	ADC39187	Adc39187 Novel hum
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ALIGNMENTS

RESULT 1

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ID AAD00521 standard; cdna; 897 BP.

XX AAD00521;

AC AAD00521;

DT 29-AUG-2000 (first entry)

XX Human adenine nucleotide translocator ANT3 CDNA.

DE Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; neurotoxic;
KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW mitochondrial diabetes and deafness; hyperproliferative disorder;
KW myoclonic epilepsy red ragged fibre syndrome; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Key 1..897

FT CDS /tag= a

FT FT /product= "ANT3"

XX WO200026370-A2.

PN 11-MAY-2000.

PD 11-MAY-2000.

XX 11-MAY-2000.

XX New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (WPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused
PT to energy transfer molecule.
XX
PS Disclosure; Fig 1; 186pp; English.
XX
CC The present sequence encodes for human adenine nucleotide translocator-3
CC (ANT-3) protein. ANT proteins are mitochondrial permeability transition
CC (MTP) pore components responsible for mediating transport of ADP across
CC the mitochondrial inner membrane. ANT proteins interact with other
CC mitochondrial core components e.g. cyclophilins to regulate MPT. The
CC present invention relates to a novel nucleic acid expression construct
CC comprising a promoter operably linked to a polynucleotide encoding a
CC mitochondrial pore component polypeptide (e.g. ANT) fused to an energy
CC transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or
CC a FLASH sequence). The novel expression construct can alter mitochondrial
CC membrane permeability transition and/or alter the interaction between
CC mitochondrial core components. The methods are useful for screening for
CC agents that alter MPT and/or cell survival. These agents are useful for
CC the prevention or treatment of diseases associated with altered
CC mitochondrial function or dysfunctional cell survival, such as
CC Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's
CC disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis,
CC stroke, hyperproliferative disorders e.g. cancer, and deafness
XX
SQ Sequence 897 BP; 174 A; 274 C; 287 G; 162 T; 0 U; 0 Other;

Alignment Scores:
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Score: 1543.00 Matches: 298
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Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x AAS05903 (1-897)

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ID AAS16690 standard; cDNA; 897 BP.
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AC AAS16690;
XX
DT 14-FEB-2002 (first entry)
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XX
KW Human; adenine nucleotide translocator; ANT; ss;
XX
KW Mitochondrial matrix protein.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..897
XX FT /*tag= a
XX FT /product= "Adenine nucleotide translocator 3 (ANT3)"
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XX WO200185944-A2.
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XX 15-NOV-2001.
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XX 11-MAY-2001; 2001WO-US015416.
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XX 11-MAY-2000; 2000US-00569327.
XX
XX (MITO-) MITOKOR.
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW;
XX Szabo TR, Ghosh SS, Moos WH, Pei Y, Carroll AK;
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XX WPI; 2002-055598/07.
XX P-PSDB; AAU10380.
XX
XX Novel recombinant expression construct for producing adenine nucleotide
XX translocator polypeptides, comprises a regulated promoter linked to
XX nucleic acid encoding the polypeptide.
XX
XX Example 3; Fig 1; 147pp; English.
XX
XX The invention relates to a recombinant expression construct (I)
XX comprising a regulated promoter operably linked to a nucleic acid
XX encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
XX proteins mediate the exchange of ATP synthesised in the mitochondrial
XX matrix for ADP in the cytosol. (I) is useful for producing recombinant

CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (i) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the coding sequence of human ANT3
 XX

SQ Sequence 897 BP; 174 A; 274 C; 287 G; 162 T; 0 U; 0 Other;

Alignment Scores:
 Pred No.: 5.4e-172 Length: 897
 Score: 1543.00 Matches: 298
 Percent Similarity: 100.00% Conservations: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-09-811-094-33 (1-298) x AAS16690 (1-897)

Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
 Db 1 ATGACGGAACAGGCATCTCTCCGCAAGACTTCTGGCCGAGGACATCGCCGCGCC 60
 Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
 Db 61 ATCTCCAGAGCGCGTGGTCCGATCGAGCGGTCAAGTGTCTGCTGACGAGTCCAGCAC 120
 Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
 Db 121 GCCAGCAAGCAGATCGCCGCGACAGCAGTACAAAGGCGCATCGTGGACTGCATGTCCGC 180
 Qy 61 IleProLysGluGlnGlyValLeuSerPheThrArgGlyValAsnLeuAlaValIleArg 80
 Db 181 ATCCCCAAGGACGAGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
 Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 Db 241 TACTTCCCACTCAAGCCCTCAACTTCCGCTTCAAGGATAAGTACAGCAGATCTTCTCT 300
 Qy 101 GlyGlyValAspLysHisThrGlnPheThrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
 Db 301 GGGGCGGTGGACAGCACACGACGTTCTGGAGGTACTTTCGGGCAACCTGGGCTCCGC 360
 Qy 121 GlyAlaAlaGlyAlaThrSerLysCysPheValTyrProLeuAspPheAlaArgThrArg 140
 Db 361 GTGCGGCGCGGCGACCT 420
 Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 Db 421 CTGGCAGCGGACGTGGGAAAGTCAAGCAGAGCGGAGTTCGAGGCCCTGGGAGACTGC 480
 Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 Db 481 CTGTGAGAGATCACAGATCCAGCGGATCCGGGCGCTGTACAGGCGCTTCAGTGTCTC 540
 Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
 Db 541 GTGAGGCGCATCATCATCTACCGGCGCGCTCTACTTCGCGCTGTACGATACGCGCAAGGC 600
 Qy 201 MetLeuProAspProLysAsnThrHisTyrValValSerTrpMetIleAlaGlnThrVal 220
 Db 601 ATGCTCCCGACCCCAAGAACACGACATCTGTGTGAGCTGGATGATCGGCGAGACCGTG 660
 Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
 Db 661 ACGGCGGTGGCGGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720

Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260
 Db 721 CAGTCCGCGCGCAAAAGGAGCTGACATCATGTACACGGCGCACCCGCTGCTGGAGGAAG 780
 Qy 261 IlePheArgAspGluGlyValAlaPhePheLysGlyAlaTyrSerAsnValLeuArg 280
 Db 781 ATCTTCAGATGAGGGGGGCGAGCCCTTCTCAAGGGTGGTGGTCCAGCTCTCGGG 840
 Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
 Db 841 GGCATGGGGCGCGCTTCTGCTGCTGTACGACGAGCTCAAGAAGGTGATC 894

RESULT 4

AA158797
 ID AA158797 standard; cDNA; 1212 BP.
 XX
 AC AA158797;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 1000.
 XX
 KW Human; neurotrophic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR P-PSDB; AM39641.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders such
 as central nervous system injuries.
 XX
 PS Claim 1; SEQ ID NO 1000; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and the
 CC encoded polypeptides (AAW38642-AAW42213) with neurotrophic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX SQ Sequence 1212 BP; 247 A; 395 C; 356 G; 214 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8,24e-172 Length: 1212
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x AAI58797 (1-1212)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
Db 131 ATGACGGACAGCCATCTCTTCCCAAGACTTCTTGGCGGAGGATCGCCGCC 190
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 191 ATCTCCAGACGGCGTGGCTCCGATCGAGGGTCAAGCTGCTGCTGAGTCCAGCAC 250
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 251 GCCAGCAAGCAGATCGCCGCCACAGCAGTACAAGGGCATCTGGCATGTGCTCGC 310
QY 61 IleProLysGluGlnGlyValLeuSerPheThrArgGlyAsnLeuAlaAsnValleArg 80
Db 311 ATCCCCAGGAGCAGGGCGTGTCTTCTGAGGGCAACCTTGGCCAAAGCTGATTGCG 370
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 371 TACTTCCCACCTCAAGCCCTCACTTCGCTTCAGGATAGTACAGCATCTTCTG 430
QY 101 GlyGlyValAspLysHisThrGlnPheThrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 431 GGGGGCGTGGACAGCACAGCAGTCTGGAGTACTTGGCGGCAACCTGGCTCGGC 490
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 491 GGTGGCGCGGCGCGACTCTCTCTGTTGTTACCCGCTGGATTTCCGAGAACCCGC 550
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 551 CTGGCAGCGGACGTGGAAAGTCAGGCACAGCGCGAGTTCGAGGGCTGGAGACTGC 610
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 611 CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCTGTACCAAGGGCTTCAGTGTCTCC 670
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 671 GTGACGGGCATCATCATCTACGGGGCGGCTTCTCGCGGTGTACGATACGGCCAGGGC 730
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 731 ATGTCTCCCGACCCCAAGACAGCACATCATCTGTTGAGTGTGATCGCGACGCGTG 790
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgArgMetMetMet 240
Db 791 ACGGCGTGGCGGCGTGGTGTCTTCTTACCCCTTCACAGGGTGGCGGCGCATGATGATG 850
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 851 CAGTCCGGGCGCAAGAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 910
QY 261 IlePheArgAspGluGlyGlyValAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
Db 911 ATCTTCAGAGATAGGGGGGCAAGCCCTTCTCAAGGGTGGCTGCTCAACGCTCTCGCG 970
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValle 298

Db 971 GGCAATGGGGGGCGCTTTCGTGCTGTACGAGCTCAAGAAGGTGATC 1024

RESULT 5

ADB48777
ID ADB48777 standard; cDNA; 1212 BP.
XX ADB48777;
AC ADB48777;
XX 04-DEC-2003 (first entry)
DT Novel human cDNA SEQ ID NO 687.
XX
DE ss; cancer; neurodegenerative disease; human.
XX Homo sapiens.
OS
FN US2003104529-A1.
XX
PD 05-JUN-2003.
XX
PF 04-JAN-2002; 2002US-00037270.
XX
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 19-JUL-2000; 2000US-00620312.
XX
PA (ZHOU)/ ZHOU P.
PA (TANG)/ TANG Y T.
PA (LIUC)/ LIU C.
PA (ASUN)/ ASUNDI V.
PA (DRMA)/ DRMANAC R T.
XX
PI Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;
XX WPI; 2003-678194/64.
XX
PT New polynucleotide, useful for treating diseases e.g., cancer or
XX neurodegenerative diseases.
PS Claim 1; SEQ ID NO 687; 99pp; English.
XX

CC The invention relates to a polynucleotide comprising a sequence given in
CC the specification, or its mature protein-coding portion, or its
CC complement. The polynucleotide is useful for treating diseases e.g.,
CC cancer or neurodegenerative diseases and many others listed in the
CC specification. The present sequence represents a novel human cDNA. Note:
CC the sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=20030104529.
XX
SQ Sequence 1212 BP; 247 A; 395 C; 356 G; 214 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8,24e-172 Length: 1212
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-09-811-094-33 (1-298) x ADB48777 (1-1212)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
Db 131 ATGACGGACAGCCATCTCTTCCCAAGACTTCTTGGCGGAGGATCGCCGCC 190
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 191 ATCTCCAGACGGCGTGGCTCCGATCGAGGGTCAAGCTGCTGCTGAGTCCAGCAC 250
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60

251 GCCAGCAGCAGATCGCGCGCGACAGCAGTACAAAGGCGCATCGTGACTGCATTGTCCGC 310
 QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyValLeuAlaAsnValIleArg 80
 Db 311 ATCCCCAAGGAGCGGGGCTGCTCTCTCTGGAGGGGCAACCTTGCCACGTCATTCGC 370
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 Db 371 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATTAAGTACAAAGCAGATCTTCTTG 430
 QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
 Db 431 GGGGCGCTGGACAAGCACACAGCTCTCGAGGTACTTTGCGGCAACCTGGGCTTCGGC 490
 QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaA-gThrArg 140
 Db 491 GGTGCGCGCGGGGACCTCTCTCTGCTGTACCGCTGGATTTCGCCAGAACCCCGC 550
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 Db 551 CTGGCAGCGGAGCTGGGAAAGTCAAGGACAGAGCGCGAGTTCCGAGGCTGGGAGACTGC 610
 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 Db 611 CTGGTGAAGATCACCAAGTCCGAGCGCATCCGGGGCTGTACCAAGGCGCTTCAGTGTCTCC 670
 QY 181 ValGlnGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200
 Db 671 GTGCAGGCGCATCATCTACCGCGCGCGCTTCCGCGGTACGATACGGCCCAAGGCG 730
 QY 201 MetLeuProAspProLysAsnHisIleValValSerTrpMetIleAlaGlnThrVal 220
 Db 731 ATGCTCCCGGACCCCAAGAACACGCACATCGTGTGTAGCTGGATGTCGCGCAGACCGTG 790
 QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
 Db 791 ACGGCGCTGGCGGGTGTGTCTCTACCTCCCTTCACACGCGTGGCGGCGCGCATGATG 850
 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
 Db 851 CAGTCCGGCGCGCAAGAGGAGCTGACATCATGTACACGGCGCACCGTGTGTGAGGAAG 910
 QY 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
 Db 911 ATCTTCAGAGATGAGGGGGGCAAGGCTCTTCAAGGGTGTGTCTCAAGCTCTCGCG 970
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
 Db 971 GGCATGGGGGGCGCTCTGCTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1024

RESULT 6

AAI60583/c
 ID AAI60583 standard; cDNA; 2035 BP.

XX AC AAI60583;
 XX AC AAI60583;
 DT 22-OCT-2001 (first entry)
 XX Human polynucleotide SEQ ID NO 4572.
 DE Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.
 XX Homo sapiens.
 OS WO200153112-A1.
 PN 26-JUL-2001.
 PD TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATTAAGTACAAAGCAGATCTTCTCGT 1633
 XX

PF 26-DEC-2000; 2000WO-US034263.
 XX 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX WPI: 2001-442253/47.
 DR P-FSDB; AAM41427.
 XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 XX Claim 1; SEQ ID NO 4572; 10078pp; English.
 XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX Sequence 2035 BP; 398 A; 611 C; 625 G; 401 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1-7e-171 Length: 2035
 Score: 1543.00 Matches: 298
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x AAI60583 (1-2035)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAppPheLeuAlaGlyIleAlaAla 20
 Db 1932 ATGACGGAACAGCGCATCTCTTCGCAAGAGACTTCTTGGCGGAGGATCCGCCGCC 1873
 QY 21 IleSerLysThrAlaValAlaAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
 Db 1872 ATCTCCAAAGCGCGCTGCTCGATCGAGCGGGTCAAGCTGCTCTGCAGGTCCAGCAC 1813
 QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
 Db 1812 GCCAGCAAGCAGATCGCCGCCGCAAGCAGTACAAAGGCGCATCTGTGACTGTCTCGC 1753
 QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
 Db 1752 ATCCCCAAGGAGCAGGGCGTGTGTCTTCTGAGGGGCAACCTTGGCAACGTCTGCG 1693
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 Db 1692 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATTAAGTACAAAGCAGATCTTCTCGT 1633

QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
 Db 1632 CGGGCGGTGGACAGACACAGCAGTCTCGAGGTACTTTGGGGCAACCTGGCTCCGGC 1573
 QY 121 GlyAlaAlaGlyValThrSerLeuCySPheValTyrProLeuAspPheAlaArgThrArg 140
 Db 1572 GTGGCGCGCGCGACCTCTCGTTCGTGTACCCGCTGGATTTCCGAGAACCCGC 1513
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 Db 1512 CTGGCAGCGGACGTGGGAAGTCAAGCAGCAGCGGAGTTCGAGGCTCGGAGACTGC 1453
 QY 161 LeuValLysIleThrLysSerAspGlyLeuArgGlyLeuTyrGlnGlyPheSerValSer 180
 Db 1452 CTGGTGAAGATCACCAAGTCGACGCGCATCCGGGGCCCTGTACCAAGGCTTCAGTGTCTCC 1393
 QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
 Db 1392 GTGAGGGCATCATCATCTACCGGGCGGCTTCTCGCGGTGACGATACGGCCAGGGC 1333
 QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
 Db 1332 ATGCTCCCGGACCCCAAGACAGCAGCATCTCGTGTGAGCTGGATGATCGCGACCGTG 1273
 QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgAtgArgMetMetMet 240
 Db 1272 ACGGCGGTGGCGGCGTGTCTTACCCCTTCGACAGGTGCGGCGCGCATGATGATG 1213
 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
 Db 1212 CAGTCCGGCGGCAAGGAGCTGACATCATGTACACGGCCACCGTCTGACTGTGGAGGAG 1153
 QY 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
 Db 1152 ATCTTCAGATGAGGGGGGGAAGGCCCTCTCAAGGGTGGTGGTCCCAAGCTCTCTCGG 1093
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
 Db 1092 GGCATGGGGGGCGCTTCGTGCTGCTCTGATACGACGAGCTCAAGAGGTGATC 1039
 RESULT 7
 ID ABX63152 standard; cDNA; 2592 BP.
 XX AC ABX63152;
 XX DT 25-FEB-2003 (first entry)
 XX DE Human cDNA #152 differentially expressed in activated vascular tissue.
 XX KW Human; gene; ss; vascular tissue; cytosolic; atherosclerosis; cardiant;
 KW hypotensive; antidiabetic; gynaecological; vasotrophic; cerebroprotective;
 KW gene therapy; vascular disease; cancer; coronary; artery disease;
 KW hypertension; diabetes; pre-eclampsia; restenosis;
 KW ischaemia-reperfusion injury; stroke.
 XX OS Homo sapiens.
 XX PN US2002137081-A1.
 XX PD 26-SEP-2002.
 XX PF 08-JAN-2002; 2002US-00044090.
 XX PR 28-JUL-2000; 2000US-0222469P.
 XX PI 08-JAN-2001; 2001US-0260483P.
 XX PA (BAND/) BANDMAN O.
 XX PI Bandman O;
 XX WI WPI; 2003-110597/10.

XX PT Combination for diagnosing, staging, treating, or monitoring the
 PT progression of treatment of a vascular disease, e.g. atherosclerosis,
 PT comprises several cDNAs that are differentially expressed in activated
 PT vascular tissue.
 XX PS Claim 1; Page; 18pp; English.
 XX CC This invention relates to a combination comprising several cDNAs that are
 CC differentially expressed in activated vascular tissue. The invention also
 CC discloses a high throughput method for detecting differentially expressed
 CC cDNAs in a sample. The cDNAs of the invention may have
 CC antiarteriosclerotic; cytosolic; cardiant; hypotensive; antidiabetic;
 CC gynaecological; vasotrophic and cerebroprotective activities and may be
 CC used in gene therapy. The cDNAs of the invention may be used in a high-
 CC throughput methods for detecting differential expression of one or more
 CC cDNAs in a sample, or screening several molecules or compounds to
 CC identify a molecule or compound that specifically binds a cDNA of the
 CC invention. A protein encoded by the cDNA may be used to screen several
 CC molecules or compounds to identify a ligand that specifically binds to
 CC the protein, or to produce or purify an antibody to the protein that can
 CC be used to detect a protein in a sample or purify a natural or
 CC recombinant protein from a sample. The nucleotides may be useful for
 CC diagnosing, staging, treating, or monitoring the progression of treatment
 CC of a vascular disease, e.g. atherosclerosis, cancer, coronary artery
 CC disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion
 CC injury, restenosis, or stroke. The cDNAs can also be used for large-scale
 CC genetic or gene expression analysis of several new nucleic acid
 CC molecules. Antibodies to the proteins encoded by the cDNAs are useful for
 CC diagnosing pre-pathologic disorders, and chronic or acute diseases
 CC associated with abnormalities in the expression, amount or distribution
 CC of the protein. The present sequence represents a cDNA of the invention
 CC that is differentially expressed in activated vascular tissue. Note: The
 CC sequence data for this patent did not form part of the specification, but
 CC was obtained in electronic format directly from USPTO at
 CC http.segdata.uspto.gov/sequence.html?DocID=20020137081
 XX SQ Sequence 2592 BP; 520 A; 790 C; 766 G; 514 T; 0 U; 2 Other;

Alignment Scores:
 Pred. No.: 1,86e-167 Length: 2592
 Score: 1510.00 Matches: 296
 Percent Similarity: 99.33% Conservative: 2
 Best Local Similarity: 98.67% Mismatches: 0
 Query Match: 97.86% Indels: 2
 DB: 7 Gaps: 0

US-09-811-094-33 (1-298) x ABX63152 (1-2592)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIle-AlaAla 20
 Db 207 ATGACGGACAGGCCATCTCTTCGCCAAGACTTCTTGGCGGAGGCATGCGCGCGC 266
 QY 20 alleSerLysThrAlaValAlaProIleGluArg-VallysLeuLeuGlnValGlnH 40
 Db 267 CATCTCCAAAGACGGCGGTGGTCCGATCGAGGGGTCAAGCTGCTGCTGAGGTCACG 326
 QY 40 isAlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleVal 60
 Db 327 ACGCCAGCAGCAGATCGCGCGCAGCAGCGGTACAGGGCATCGTGGACTGATTTGCC 386
 QY 60 rgIleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleA 80
 Db 387 GCATCCCAAGGAGCAGGGCGTCTCTCTCTGGAGGGGCAACCTTGGCAAGTCATTC 446
 QY 80 rgTyrPheProThrGlnAlaLeuAspPheAlaPheLysAspLysTyrLysGlnIlePhe 100
 Db 447 GCTACTTCCCACTCAAGCCCTCACTTCGCCCTCAAGGATTAAGTACACAGCAGATCTTC 506
 QY 100 euGlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerG 120
 Db 507 TGGGGGGCGTGGACAAAGCACACGACGTCTTGGAGGTACTTTGGGGCAACCTGGCGCTCG 566

```
QY 120 lyGlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrA 140
Db 567 GCGGTGCGCGCGCGACCTCCCTCTCGTGTATCCCGCTGGATTTGCCAGAACCC 626
QY 140 rgLeuAlaAlaAspValGlyysSerGlyThrGluArgGluPheArgGlyLeuGlyAspC 160
Db 627 GCCTGGCAGCGAGCGTGGGAAGTACAGCACAGAGCGGAGTTCGAGGCGCTGGAGACT 686
QY 160 ysLeuValIysIleThrIysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValS 180
Db 687 GCCTGTGAAGATCACCAAGTCCGACGCGCATCCGGGCGCTGTACCAGGGCTTCAGTGTCT 746
QY 180 erValGlnGlyIleIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaIysG 200
Db 747 CCGTCAGCGCATCATCATCTACCGGGCGGCGTACTTTCGGCGTGTACGATACGCGCCAAAG 806
QY 200 lyMetLeuProAspProIysAsnThrHisIleValValSerTyrMetIleAlaGlnThrV 220
Db 807 GCATGCTCCCGACCCCAAGACACGACATCGTGTGAGTGTGATCGCGGACCG 866
QY 220 alThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetM 240
Db 867 TCACGGCGGTGCGCGCGTGTCTTACCCCTTCGACACGCGTCCGCGCGCGCATGATGA 926
QY 240 etGlnSerGlyArgGlyGlyAlaAspIleMetTyrThrGlyThrValAspCysThrPargL 260
Db 927 TGCAGTCCGGCGCGCAAGAGAGTGCATCATGTACACGGGCGACGTCGACTGTGGAGGA 986
QY 260 ysIlePheArgAspGluGlyGlyIysAlaPhePheIysGlyAlaTyrSerAsnValLeuA 280
Db 987 AGATCTTCAGAGATGAGGGGCGGAGGCGCTTCTTCAAGGGTGTGCTGCCAAGCTCTGTC 1046
QY 280 rgGlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuIysIysValIle 298
Db 1047 GGGCATCGGGGCGCGCTTCGTGTGTCTGTGTACGAGCTCAAGAGGTGATC 1102
RESULT 8
ID AAL48635
XX AAL48635 standard, cDNA; 1225 BP.
AC AAL48635;
XX
XX
DT 11-OCT-2002 (first entry)
XX
DE Human insulin receptor signaling modifier cDNA SEQ ID NO: 53.
KW Human; insulin receptor signaling; insulin receptor signaling modifier;
KW ISM; diabetes; metabolic syndrome; antidiabetic; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200255664-A2.
XX
PD 18-JUL-2002.
XX
PF 11-JAN-2002; 2002WO-US001048.
XX
XX 12-JAN-2001; 2001US-0261226P.
PR 12-JAN-2001; 2001US-0261303P.
PR 12-JAN-2001; 2001US-0261304P.
PR 12-JAN-2001; 2001US-0261335P.
PR 12-JAN-2001; 2001US-0261336P.
PR 12-JAN-2001; 2001US-0261361P.
PR 12-JAN-2001; 2001US-0261456P.
PR 12-JAN-2001; 2001US-0261457P.
PR 12-JAN-2001; 2001US-0261458P.
PR 12-JAN-2001; 2001US-0261459P.
PR 12-JAN-2001; 2001US-0261461P.
PR 12-JAN-2001; 2001US-0261518P.
PR 12-JAN-2001; 2001US-0261531P.
PR 12-JAN-2001; 2001US-0261532P.
PR 12-JAN-2001; 2001US-0261589P.
PR 12-JAN-2001; 2001US-0261590P.
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PR 12-JAN-2001; 2001US-0261694P.
PR 12-JAN-2001; 2001US-0261695P.
PR 12-JAN-2001; 2001US-0261697P.
XX
XX (EXEL-) EXELIXIS INC.
XX
XX Seidel-Dugan C, Ferguson KC, Kidd T;
XX
XX WPI; 2002-599564/64.
XX P-PSDB; AA018516.
XX
XX Identifying an insulin receptor signaling modulator, useful as drug
XX targets for treating diabetes or metabolic disorders, comprises
XX contacting an assay system comprising insulin receptor signaling
XX modifiers with a test agent.
XX
XX Disclosure; Page 159-160; 232pp; English.
XX
XX The present invention relates to a method of identifying a candidate
XX insulin receptor (INR) signaling modulating agent, involving contacting
XX an assay system comprising an insulin receptor signaling modifier (ISM)
XX polypeptide or nucleic acid with a test agent, and detecting a test agent
XX biased activity of the assay system. The method is useful for
XX identifying candidate INR signaling modulating agents. ISM genes may be
XX used as drug targets for treatment of disorders related to INR signaling
XX such as diabetes or metabolic syndrome. ISM nucleic acids and
XX polypeptides are useful for identifying and testing agents that modulate
XX ISM function and for other applications related to the involvement of ISM
XX in INR signaling, and for identifying subjects having a predisposition to
XX such diseases associated with INR signaling. The present sequence is an
XX ISM coding sequence described in the exemplification of the invention
XX
XX SQ Sequence 1225 BP; 295 A; 300 C; 307 G; 323 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2,27e-162 Length: 1225
XX Score: 1463.00 Matches: 275
XX Percent Similarity: 97.30% Conservative: 13
XX Best Local Similarity: 92.91% Mismatches: 8
XX Query Match: 94.82% Indels: 0
XX DB: Gaps: 0
XX
XX US-09-811-094-33 (1-299) x AAL48635 (1-1225)
XX
XX QY 1 MetThrGluGlnAlaIleSerPheAlaIysAspPheLeuAlaGlyIleAlaAlaA 20
XX
XX Db 69 ATGACAGATGCGCTGTGTCTTCGCCAAGGACTTCCTGGCAGGTGGAGTGGCGCAGCC 128
XX
XX QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
XX
XX Db 129 ATCTCCAAAGACGGGTAGCGCCATCGAGCGGGTCAAGCTGCTGCTCAGGTGCGAGCAT 188
XX
XX QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
XX
XX Db 189 GCCAGCAGCAGATCACTGCAGATAAGCAATACAAAGGCATTATAGATCGGTGCTCGT 248
XX
XX QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
XX
XX Db 249 ATTCCCAAGGACGAGGAGTTCCTCTTCTGGCGCGGTAACTGGCCAAATGTATCACA 308
XX
XX QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
XX
XX Db 309 TACTTCCCGCCAGGCTCTTAACCTTCGCTTCAAGAGATAATACAGCAGATCTTCTCG 368
XX
XX QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
XX
XX Db 369 GGTGGTGTGGACACAGAGAACCCAGTTTGGCGCTACTTTGCAGGGAATCTGGCATCGGT 428
XX
XX QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
XX
XX Db 429 GGTGCCGCGAGGGGCGACATCCCTGTGTTTGTGTACCCCTCTTGATTTTGGCCGACCCGT 488
XX
XX 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
```

Db 489 CTAGCAGCTGATGGTAAAGCTGGAGCTGAAGGGAATTCGAGGCTCGGTGACTGC 548
QY 161 LeuValLysIleThrLysSerAspGlyLeuArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 549 CTGGTAAAGATACAAATCTCATGGGATTAAGGGCTGTACCAAGGCTTTAAAGCTGTCT 608
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 609 GTGCAGGATATTATCATCTACCGAGCGGCTTCTCGGTATCTATGACACTGCAAGGGA 668
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 669 ATGGCTTCGGGATCCCAAGAACACTCACATCGTCATCGATCGATCGATCGATCGATCG 728
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 729 ACTGCTGTGCGGGTGAATCTTCCATTCATTTGACCGCTTTCGGCGCGGATGATGATG 788
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 789 CAGTCAGGGCGCAAGGAAGTACATCATGACAGGACGCTTGACTGTGGCGGAAG 848
QY 261 IlePheArgAspGlnGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
Db 849 ATTGCTCGTGATGAAGGAGGCAAGCTTTTTCAGGGTGCATGTCATGTCATGTCATG 908
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
Db 909 GGCATGGTGGTGGCTTTTGTGCTTGTCTGTATGATGATGAATCAGAGAG 956

RESULT 9
AAD00520
ID AAD00520 standard; cDNA; 897 BP.
AC
XX
XX
DT 29-AUG-2000 (first entry)
XX
DE Human adenine nucleotide translocator ANT2 cDNA.
XX
KW Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; norepinephrine;
KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW antipsychotic; neuroprotective; therapeutic; screening; psoriasis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW mitochondrial diabetes and deafness; hyperproliferative disorder;
KW myoclonic epilepsy red ragged fibre syndrome; ss.

OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
CDS 1..897
FT /*tag= a
FT /product= "ANT2"
XX
XX WO2000026370-A2.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-US025883.
XX
XX 03-NOV-1998; 98US-00185904.
PR 08-SEP-1999; 99US-00393441.
XX
XX (MITO-) MITOKOR.
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW;
PI Szabo TR, Ghosh SS;
XX

DR WPI; 2000-365619/31.
DR P-PSDB; AAY71032.
XX
PT Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
FT against mitochondrial disease.
XX
XX Example 1; Page 165-166; 175pp; English.
XX
CC The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine di/tri-
CC phosphates across the mitochondrial inner membrane and also serves as an
CC important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's
CC hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy,
CC lactic acidosis and stroke (MELAS), hyperproliferative disorders,
CC mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red
CC ragged fibre syndrome. The present sequence is a cDNA encoding adenine
CC nucleotide translocator ANT2 from human brain
XX
SQ Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.69e-161 Length: 897
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservative: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
DB: 3 Gaps: 0

US-09-811-094-33 (1-298) x AAD00520 (1-897)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
Db 1 ATGACAGATGCCGATCTTCTTCCGACAGGACTTCTTCCGAGGAGGAGTGGCCGAGCC 60
QY 21 IleSerLysThrAlaValAlaProfileGluArgValLysLeuLeuGlnValGlnHis 40
Db 61 ATCTCCAGACGGCGGTAGCGCCATCGAGCGGTCAAGCTGCTGTCAGGTGAGCAT 120
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 121 GCCAGACAGCATCACTGCAGATAGCAATCAAGGCAATATAGACTGCGGTGCTCGT 180
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 181 ATTCCCAAGGAGCAGGAGTCTTCTTCTTCCGCGGTAACCTGGCCATATGTCATCAGA 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 241 TACTTCCCGACCGAGGCTCTTAACCTGCGCTTCAAGATAAATACAGCAGATCTTCTCG 300
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 301 GGTGGTGTGCAACAAGAGAACCCAGTTTGGCGCTACTTTCAGGGAATCTGCAATCGGT 360
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 361 GGTGCGCAGGCGCCACATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 421 CTAGACAGCTGATGTGGGTAAAGCTGAGCTGAAGGGAATTCGAGGCTCGGTGACTGC 480
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180

QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
 Db 661 ACTGCTGTTGCCGGGTGTACTTCTCATCCATTGACACCGTTCCGCCGCCGATGATG 720
 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
 Db 721 CAGTCAGGCGCAAGAACTGACATCATGTACACAGGCACCTTGACTGCTGGCGGAAG 780
 QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
 Db 781 ATTGCTCGTGATCAAGAGGCAAGCTTTTCAAGGGTGCATGCTCCAATGTTCTCAGA 840
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
 Db 841 GGCATGGGTGGTCTTTTGCTTGTGTATGAAATCAAGAAG 888

RESULT 11

AAS16689

ID AAS16689 standard; cDNA; 897 BP.

XX AAS16689;

DT 14-FEB-2002 (first entry)

DE DNA encoding human adenine nucleotide translocator 2 (ANT2).

KW Human; adenine nucleotide translocator; ANT; ss;

KW mitochondrial matrix protein.

XX Homo sapiens.

FH Key Location/Qualifiers

FT 1..897

FT /*tag= a

FT /product= "Adenine nucleotide translocator 2 (ANT2)"

XX WO200185944-A2.

XX 15-NOV-2001.

XX 11-MAY-2001; 2001WO-US015416.

XX 11-MAY-2000; 2000US-00569327.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW;

PI Szabo TR, Ghosh SS, Moos WH, Pei Y, Carroll AK;

XX WPI; 2002-055598/07.

DR P-PSDB; AAU10379.

XX Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide.

PS Example 1; Fig 1; 147bp; English.

XX The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesized in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also

CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the coding sequence of human ANT2

SQ Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.69e-161 Length: 897
 Score: 1454.00 Matches: 274
 Percent Similarity: 96.96% Conservative: 13
 Best Local Similarity: 92.57% Mismatches: 9
 Query Match: 94.23% Indels: 0
 DB: 6 Gaps: 0

US-09-811-094-33 (1-298) x AAS16689 (1-897)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
 Db 1 ATGACAGATCCGCGATGTCTTCGCCAAGGATTTCTGCAGTGGAGTGGCGGAGCC 60
 QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
 Db 61 ATCTCCAAGACGGCGGTAGCGCCATCGAGCGGTCAGCTGCTGTCAGGTGCAGCAT 120
 QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
 Db 121 GCCAGCAGCAGATCACTGCAGATAAGCAATACAAAGGCAATATAGACTCGGTGCGGT 180
 QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
 Db 181 ATTCCCAAGGACGAGGAAGTTCTGTCCTTCTGGCGGGTAACCTGGCCATGTCATCAGA 240
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 Db 241 TACTTCCCCACCCAGGCTCTTAACCTTCGCCCTTCAAGAGATAAATACAAAGCAGATCTTCTTG 300
 QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
 Db 301 GGTGGTGGACAGAGAACCCAGTTTGGCGCTACTTTGCAGGGAAATCTGGCATCGGGT 360
 QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
 Db 361 GGTGGCGGCGGCGCACATCCCTGTGTTTGTGTACCTCTTGATTTTCCCGTACCGCT 420
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 Db 421 CTAGCAGCTGATGTGGTTAAGCTGGAGCTAAAGGGAATTCGAGGCTTCGCTGACTGC 480
 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 Db 481 CTGTTTAAGATCTACAAATCTGATGGATTAAAGGCTCTGACCAAGGCTTTAACGTGTCT 540
 QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
 Db 541 GTGAGGGTATTATCATCTACCGAGCGGCTACTTGGTATCTATCATCATGCACTGCAAGGGA 600
 QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTyrMetIleAlaGlnThrVal 220
 Db 601 ATGCTTCCGATCCCAAGAACACTCACATCGTCACTGCTGATGATGCCAGACTGTCT 660
 QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
 Db 661 ACTGCTGTTGGCGGGTGTACTTCTTATCATTTGACACCGTTCGCCGCCGATGATGATG 720
 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
 Db 721 CAGTCAGGCGCAAGAACTGACATCATGTACAGGCACCGCTTGACTGCTGGCGGAAG 780
 QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
 Db 781 ATTGCTCGTGATCAAGAGGCAAGCTTTTCAAGGGTGCATGCTCCAATGTTCTCAGA 840
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296

Wed Aug 18 16:42:48 2004

Db	841	GGCATGGGTGGTCTTTTGTCTTGTCTTGTATGAAATCAAGAG	888
RESULT 12			
ABK63420			
ID	ABK63420	standard; cDNA; 1196 BP.	
XX	AC	ABK63420;	
XX	AC		
XX	DT	18-JUN-2002 (first entry)	
XX	XX		
XX	XX	Rat sequence differentially expressed in response to a hepatotoxin #1327.	
DE	XX		
XX	XX	Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;	
KW	XX	differential expression; centrilobular necrosis; steatosis.	
KW	XX		
XX	OS	Rattus norvegicus.	
XX	XX		
XX	XX	WO200210453-A2.	
XX	XX		
PD	XX	07-FEB-2002.	
XX	XX		
XX	XX	30-JUL-2001; 2001WO-US023872.	
XX	XX		
PR	XX	31-JUL-2000; 2000US-0222040P.	
PR	XX	02-NOV-2000; 2000US-0244880P.	
PR	XX	11-MAY-2001; 2001US-0250029P.	
PR	XX	15-MAY-2001; 2001US-0290645P.	
PR	XX	22-MAY-2001; 2001US-0292336P.	
PR	XX	06-JUN-2001; 2001US-0295798P.	
PR	XX	13-JUN-2001; 2001US-0297457P.	
PR	XX	19-JUN-2001; 2001US-0298884P.	
PR	XX	09-JUL-2001; 2001US-0303459P.	
XX	XX	(GENE-) GENE LOGIC INC.	
XX	PA		
XX	PI	Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;	
XX	PI		
XX	XX	WPI; 2002-241625/29.	
DR	XX		
XX	XX	Predicting toxic effects of compounds or the progression of these toxic	
PT	XX	effects by determining the changes in gene expression in tissues or cells	
PT	XX	exposed to the toxin and comparing these to gene expression in unexposed	
PT	XX	tissues or cells.	
XX	XX	Claim 1; SEQ ID NO 1327; 239pp; English.	
XX	XX		
CC	XX	The invention relates to methods for predicting toxic effects of	
CC	XX	compounds or the progression of these toxic effects by determining the	
CC	XX	global changes in gene expression in tissues or cells exposed to the	
CC	XX	toxin and comparing these to gene expression in unexposed tissues or	
CC	XX	cells. Also included are methods of predicting at least one toxic effect	
CC	XX	of a compound or progression of a toxic effect, preferably the	
CC	XX	hepatotoxicity of a compound, comprising detecting the level of	
CC	XX	expression in a tissue or cell sample exposed to the compound of two or	
CC	XX	more genes listed in the specification, where differential expression of	
CC	XX	the genes is indicative of at least one toxic effect or progression. The	
CC	XX	method can also be used to identify an agent which modulates the toxic	
CC	XX	response and predict cellular pathways that a compound modulates in a	
CC	XX	cell. The methods utilize a set of at least two probes (on a solid	
CC	XX	support in kit form), where each of the probes comprises a sequence that	
CC	XX	specifically hybridizes to a gene listed in the specification, a computer	
CC	XX	system comprising a database containing information identifying the	
CC	XX	expression level in a tissue or cell sample exposed to a hepatotoxin of a	
CC	XX	set of genes comprising at least two genes listed in the specification,	
CC	XX	and a user interface to view the information used to present information,	
CC	XX	identifying the expression level in a tissue or cell of at least one gene	
CC	XX	listed in the specification. The method is useful for elucidating global	
CC	XX	changes in gene expression and for identifying toxicity markers in	
CC	XX	tissues or cell exposed to a known toxin. The genes may be used as	
CC	XX	toxicity markers in drug screening and toxicity assays. The genes and	
CC	XX	gene expression information may be used as diagnostic markers for the	
CC	XX	prediction or identification of the physiological state of tissue or cell	
CC	XX	sample that has been exposed to a compound or agent. Hepatotoxicity is	

CC	characterised by centrilobular necrosis and steatosis. The present		
CC	sequence is an expressed sequence tag (EST) or cDNA derived from a gene		
CC	which is differentially expressed in response to a hepatotoxic agent		
XX			
SQ	Sequence 1196 BP; 295 A; 279 C; 326 G; 296 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	8,73e-158	Length:	1196
Score:	1424.00	Matches:	267
Percent Similarity:	95.64%	Conservative:	18
Best Local Similarity:	89.60%	Mismatches:	13
Query Match:	92.29%	Indels:	0
DB:	6	Gaps:	0
US-09-811-094-33 (1-298) x ABK63420 (1-1196)			
QY	1	MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla	20
Db	76	ATGGGGATCAGGCTTTCAGGCTTCTTAAGGACTTCTTGGCAGGTGGCATCCGCGCGCC	135
QY	21	IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis	40
Db	136	GTCTCCAGACCGCGTCCCGGATCGAGAGGTCAACTGCTGCTGCAGGTCACGAT	195
QY	41	AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg	60
Db	196	GCCAGCAACAGATCAGTGCAGAGAAACAGTACAAAGGCATCATTTGTTGTCTGAGA	255
QY	61	IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg	80
Db	256	ATCCCAAGAGCAGGCGCTTCTCTCTCTGGAGGGTAACCTGGCCCAAGTATCCGG	315
QY	81	TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu	100
Db	316	TACTTCCCAACCAAGCTCTCACTTCGCTTCAAGGACAAAGTACAAGCAGATCTCTGT	375
QY	101	GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly	120
Db	376	CGAGGTGGATCGTCATAAGCAGTTCGGCGCTACTTCGCTGTAACCTGGCTCTCTGT	435
QY	121	GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg	140
Db	436	GGGGCAGCTGGGGCTACCTCCCTCTGCTTACCCACCTGGACTTGTAGGACCAAG	495
QY	141	LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys	160
Db	496	CTGGTCCCGACGTGGCAAGGATCTTCCACGCGTGAGTTCAATGGCTGGTGACTGT	555
QY	161	LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer	180
Db	556	CTCACCAGATCTCAAGTCTGATGGCTGAAGGGTCTCTACCAAGGTTTCAGTGTCTCT	615
QY	181	ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly	200
Db	616	GTGAGGCGATCATCATCTACAGAGCTGCTACTTCTCGGAGTCTATGACACTCCCAAGGG	675
QY	201	MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal	220
Db	676	ATGCTCCAGACCCCAAGAAATGTGCACATTATTGTGAGCTGGATGATGCCAGAGTGTG	735
QY	221	ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet	240
Db	736	ACAGCGCTGGGGGCTGTGCTCTTCCATCCATTTGACACTGTCGCTAGGATGATGATG	795
QY	241	GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys	260
Db	796	CAGTCTGGCGGAAGGGGCTGATATTATGTACCGGGACAGTTCAGTCTGGAGGAAG	855
QY	261	IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyIleAlaTrpSerAsnValLeuArg	280
Db	856	ATTGCAAAAGATGAAGGACGCAAGCTTCTTCAAAGGTGCTTGTGTCACACGCTACTGAGA	915
QY	281	GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle	298

OS Rattus norvegicus.
 XX WO2003065993-A2.
 PN 14-AUG-2003.
 PD 04-FEB-2003; 2003WO-US003482.
 PF 04-FEB-2002; 2002US-0353171P.
 PR 13-MAR-2002; 2002US-0363534P.
 PR 08-APR-2002; 2002US-0370248P.
 PR 10-APR-2002; 2002US-0371134P.
 PR 10-APR-2002; 2002US-0371135P.
 PR 10-APR-2002; 2002US-0371150P.
 PR 11-APR-2002; 2002US-0371413P.
 PR 19-APR-2002; 2002US-0373601P.
 PR 19-APR-2002; 2002US-0373602P.
 PR 22-APR-2002; 2002US-0374139P.
 PR 08-MAY-2002; 2002US-0378370P.
 PR 09-MAY-2002; 2002US-0378652P.
 PR 09-MAY-2002; 2002US-0378653P.
 PR 09-MAY-2002; 2002US-0378655P.
 PR 09-JUN-2002; 2002US-0394230P.
 PR 09-JUL-2002; 2002US-0394235P.
 PR 04-SEP-2002; 2002US-0407688P.
 PR 28-JAN-2003; 2003US-0442900P.
 XX (GENE-) GENE LOGIC INC.
 PA Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
 XX Elashoff M;
 PI WPI; 2003-731472/69.
 DR
 XX
 PT Determining if a compound induces a toxic effect on a tissue or cell, for
 PT identifying hepatotoxic compounds, comprises comparing a gene expression
 PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
 PT mean values.
 PS Claim 44; SEQ ID NO 2883; 874pp; English.
 XX
 CC The present invention describes a method for determining whether a
 CC compound induces a toxic effect on a tissue or cell. The method comprises
 CC preparing a gene expression profile of a tissue or cell sample exposed to
 CC the compound, and comparing the gene expression profile to a database
 CC comprising data or information on the Tox mean and non-Tox mean value.
 CC The method is useful for predicting or identifying at least one toxic
 CC effect, particularly hepatotoxicity, of a test or unknown compound. The
 CC genes listed in the specification are useful as diagnostic or toxicity
 CC markers for the prediction or identification of the physiological state
 CC of tissue or cell sample that has been exposed to a compound, or to
 CC identify or predict the toxic effects of a compound or an agent. These
 CC may also be used as markers for monitoring toxicity progression or for
 CC drug screening. The present sequence represents a primary rat hepatocyte
 CC toxicity modelling related gene sequence from the present invention.
 XX
 SQ Sequence 1196 BP; 295 A; 279 C; 326 G; 296 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.73e-158 Length: 1196
 Score: 1424.00 Matches: 267
 Percent Similarity: 95.64% Conservativity: 18
 Best Local Similarity: 89.60% Mismatches: 13
 Query Match: 92.29% Indels: 0
 DB: 9 Gaps: 0
 US-09-811-094-33 (1-298) x ADB52341 (1-1196)
 Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAala 20
 DB 76 ATGGGGGATCAGGCTTTCAGCTTCTTAAGGACTTCTGGCAGGTGCATCGCGCGGCC 135
 Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnHis 40

Db 136 GTCTCCAAGACCGCGGTGCGCCCGATGAGAGGGTCAAACTGCTGTCGAGTCCAGCAT 195
 Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnIleValAspCysIleValArg 60
 Db 196 GCCAGCAACAGATCAGTGCAGAGAAACAGTACAAAGGCATCATTTGTTGCTGAGA 255
 Qy 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
 Db 256 ATCCCAAGGAGCAGGGGCTTCTCTCTTCGAGGGGTAACTGGCCCAACGTCATCCGG 315
 Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 Db 316 TACTTCCCCACCCCAAGCTCTCAACTTCGCTTCAAGGACAAAGTACAGCAGATCTTCTG 375
 Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
 Db 376 GGAGGTGGATCGTCATACAGCAGTCTTGGCGCTTACTTCGCTGAACCTGGCCTCTGGT 435
 Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
 Db 436 GGGGCGAGCTGGGGCTACCTCCTCTCTCTTACCCACTGGACCTTGTAGACCAAG 495
 Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 Db 496 CTGGCTGCCGACGTGGGCAAGGATCTTCCAGCGTGAGTTCATGGGCTGGTGACTGT 555
 Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 Db 556 CTCACCAAGATCTTCAAGTCTGATGGCTGAAGGGTCTCTACACAGGGTTTCAGTGTCTCT 615
 Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
 Db 616 GTGCGAGGCAATCATCTACAGAGCTGCCTTCTCGAGTCTATGACACTGCCAAGGG 675
 Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
 Db 676 ATGCTGCTCCAGACCCCAAGATGTGCACATTATTGTGAGCTGGATGATGCCAGAGTGTG 735
 Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
 Db 736 ACAGCGGTGGCGGGCTGTCTCTATCCATTTGACACTGTCCTGCTGAGTATGATGATG 795
 Qy 241 GlnSerGlyArgLysGlyValAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
 Db 796 CAGTCTGCCGGAAGAGGGGCTGATATATGATACACGGGACAGTTCAGTCTGGAGGAAG 855
 Qy 261 IlePheArgAspGluGlyGlyAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
 Db 856 ATTGCAAAAGATGAAGGACGCAAAAGCTTCTTCAAGGTGCTTGGTCCCAAGTACTGAGA 915
 Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
 Db 916 GCATGGGGGGTGGCTTTTGTATTGATGATGATGATGATGATGATGATGATGATG 969

RESULT 15
 ACC46652
 ID ACC46652 standard; cDNA; 2213 BP.
 XX ACC46652;
 AC ACC46652;
 XX
 DT 02-JUN-2003 (first entry)
 XX
 DE Human dithp organelle-associated protein-encoding cDNA.
 XX
 XX Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
 KW cancer; cell proliferative disorder; autoimmune disorder;
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 KW neurological disorder; gastrointestinal disorder; transport disorder;
 KW connective tissue disorder; drug screening; proteome analysis;
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 KW disease model; toxicological testing; transcript imaging;
 KW organelle-associated protein; gene; ss.

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XX OS Homo sapiens.
XX PN WO200297031-A2.
XX PD 05-DEC-2002.
XX PF 27-MAR-2002; 2002WO-US010056.
XX PR 28-MAR-2001; 2001US-0279619P.
XX PR 29-MAR-2001; 2001US-0280067P.
XX PR 29-MAR-2001; 2001US-0280068P.
XX PR 16-MAY-2001; 2001US-0291280P.
XX PR 17-MAY-2001; 2001US-0291829P.
XX PR 17-MAY-2001; 2001US-0291849P.
XX PR 19-JUN-2001; 2001US-0299428P.
XX PR 20-JUN-2001; 2001US-0299776P.
XX PR 20-JUN-2001; 2001US-0300001P.
XX (INCY-) INCYTE GENOMICS INC.
XX PA Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
XX PI Dufour GE, Hillman JL, Yu JY, Tuason C, Yap PE, Amshey SR;
XX PI Daugherty SC, Dam TC, Liu TP, Nguyen DA, Kleefeld Y, Gerstin EH;
XX PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
XX PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX WPI: 2003-129518/12.
XX DR P-PSDB; ABR41715.
XX PT Novel human diagnostic and therapeutic polypeptide useful for identifying
XX PT test compound which specifically binds to a polypeptide encoded by human
XX PT diagnostic and therapeutic polynucleotide, and to induce antibodies.
XX PS Claim 2; SEQ ID NO 573; 591pp; English.
XX CC The invention relates to novel human diagnostic and therapeutic
XX CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
XX CC proteins (DITHP: ABR41136-ABR41812). The invention also relates to
XX CC polynucleotide sequences at least 90% identical to the dithp cDNA
XX CC sequences of the invention; recombinant vectors, host cells and
XX CC transgenic organisms comprising a dithp nucleic acid sequence; the
XX CC recombinant production of DITHP proteins; antibodies specific for DITHP
XX CC proteins; microarrays comprising dithp nucleic acid sequences; methods of
XX CC detecting dithp nucleotide and protein sequences; methods of screening
XX CC for compounds which specifically bind a DITHP protein; and methods of
XX CC assessing the toxicity of test compounds using a dithp hybridisation
XX CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
XX CC diagnosis of a wide variety of conditions including cancer and other cell
XX CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
XX CC viral, fungal or parasitic infections; hormonal disorders; metabolic
XX CC disorders; neurological disorders; gastrointestinal disorders; transport
XX CC disorders; and connective tissue disorders. They may also be used to
XX CC screen for modulators of protein activity or gene expression. DITHP
XX CC proteins can additionally be used in analysis of the proteome of a tissue
XX CC or cell type and to induce antibodies. The dithp nucleic acids are
XX CC additionally useful in somatic or germline gene therapy of the disorders
XX CC mentioned above, as a source of antisense sequences, as a source of
XX CC probes and primers, in genotyping and identification of individuals, in
XX CC the generation of transgenic animal models of human disease or knock in
XX CC humanised animals, in toxicological testing, and in transcript imaging.
XX CC The present sequence represents a dithp cDNA encoding a DITHP protein
XX CC which is an organelle-associated protein. Note: The sequence data for
XX CC this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 2213 BP; 422 A; 751 C; 633 G; 407 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.05e-156 Length: 2213
Score: 1418.00 Matches: 277
Percent Similarity: 96.22% Conservative: 3

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Best Local Similarity: 95.19% Mismatches: 5
Query Match: 91.90% Indels: 6
DB: 7 Gaps: 2

US-09-811-094-33 (1-298) x ACC46652 (1-2213)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
DB 206 ATGACGGAAACAGGCCATCTCTTCGCAAGACTTCTTGCCGAGGAGCATCGCGCGGCC 265
QY 21 IleSerIysThrAlaValAlaProIleGluArgValIysLeuLeuGlnValGlnHis 40
DB 266 ATCTCCAAAGACGCGCTGCTCGATCGAGCGGCTCAAGTCTGCTGAGGTCCAGCAC 325
QY 41 AlaSerIysGlnIleAlaAlaLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 326 GCCAGCAAGCAGATCGCGCGCAAGAGTACAAGGGCATCGTGACTGCAATGTGCGCG 385
QY 61 IleProIysGluGlnGlyValLeuSerPheThrArgGlyAsnLeuAlaValIleArg 80
DB 386 ATCCCAAGGAGCAGCGCTGCTCTCTTGAGGGGCAAGCTTCCCAACGTCATTCGC 445
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 446 TACTTCCCACACTCAAGCCCTCAACTTCGCTTCAAGGATAAGTACAGCAGATCTTCCTG 505
QY 101 GlyGlyValAspLysHisThrGlnPheThrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 506 GGGGGCGGTGGACAAGCACACGAGTCTCTGAGGTACTTTTCGGGGCAACCTGCGCTCGGC 565
QY 121 GlyAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 626 CTGGCAGCGAGCGTGGGAAAGTCAGGCACAGAGCGGAGTTCGAGGCGCTGGAGACTGC 685
QY 161 LeuValIysIleThrIysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 686 CTGGTGAAGATCAACCAAGTCCGACGACATCCGGGGCTGTACCCAGGGCTTCAGTGTCTCC 745
QY 181 ValGlnGlyIleIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 746 GTCCAGGCGCATCATCATCTACCGGGCGGCTACTTCGGCGTGTACGATACGCCAAGGCG 805
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
DB 806 ATGCTCCCGACCCCAAGAACACGACATCGTGGTGGAGTGGATGATCGCGCAGACCGTG 865
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgArgMetMetMet 240
DB 866 ACGGCGGTGGCGCGCTGTGTCTTACCCCTTCGACACGCTGGCGCGGCGCATGATGATG 925
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
DB 926 CAGTCCGGGCGCAAGAGGCTGACATCATGTACACGGGACCGCTGCTGCTGTTGGAGGAAG 985
QY 261 IlePheArgAspGluGlyGlyValAlaPhePheLysGlyAla---Trp----- 275
DB 986 ATCTTCAGAGATGAGGGGGCAAGGCCCTTCTTCAGGGGTTCACACTGGAAACAAGCGAGC 1045
QY 276 ---SerAsnValLeuArgGlyMetGlyGlyAla 285
DB 1046 CTGCGGACGCGCCCTCGAGGGGCTCACCTTCTGCA 1078

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Search completed: August 17, 2004, 19:33:52
Job time : 489 secs

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QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAala 20
Db 1 ATGACGGAAACAGGCGCATCTCTTCCCAAGACTTCTTGGCCGAGGAGCATCGCCGCCGCC 60
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuLeuGlnValGlnHis 40
Db 61 ATCTCCAGAGCGCGCTGGCTCCGATCGAGCGGCTCAAGCTGCTGCTGAGTCCAGCAC 120
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 121 GCCAGCAAGCAGATCGCCGCCGACAGCAGTACAAGGGCATCGTGGACTGCTGATTCCTG 180
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 181 ATCCCAAGGAGCGGCGTCTCTCTTGGAGGGGCAACCTTGGCAACGTCATTCGC 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 241 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAAGTACAAGCAGATCTTCTCTG 300
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 301 GGGGGCGTGGACAGACACACAGTCTTGGAGGTACTTTCGGGCAACCTGGGCTCCGCC 360
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 361 GGTGGCGCGCGGACCTCTCTCTGCTGTGTACCGCTGGATTTTGCAGAACCCGC 420
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGlnArgGluPheArgGlyLeuGlyAspCys 160
Db 421 CTGCAGCGGAGTGGGAAAGTACAGGACAGCGCGAGTTCGGAGGCTTGGGAGACTGC 480
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 481 CTGTGTGAATCACCAAGTCCGACCGCATCCGGGCTGTACCGAGGCTTCAAGTGTCTC 540
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 541 GTGCAGGCGCATCATCATACCGGGCGGCTACTTTCGGCGTGTACGATACGCGCAAGGC 600
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 601 ATGCTCCCGGACCCCAAGACACGACATCGTGTGAGCTGGATGATCGCGCAGACCGTG 660
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 661 ACGGCCGTGGCGCGGTGTCTCTACCCCTTCGACACGTCGTCGCGCGCATGATGATG 720
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 721 CAGTCCCGCGGCAAGAGCTGATCATATGACACGCGGACCGCTCGACTGTTGGAGGAAG 780
QY 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
Db 781 ATCTTCAGAGATGAGGGGGGCAAGGCCCTTCTTCAAGGGTCTGGTTCACAGCTCTGCGG 840
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGlnLeuLysLysValIle 298
Db 841 GGATGCGGGCGCGCTTCTGCTGCTCTGTACGAGAGCTCAAGAGGTGATC 894
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RESULT 2

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US-09-620-312D-687
; Sequence 687, Application US/09620312D
; Patent No. 659662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyen
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
```

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; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Danrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 659662el Nucleic Acids and
; TITLE OF INVENTION: Polyptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 687
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (131)..(1027)
US-09-620-312D-687

Alignment Scores:
Pred. No.: 1,37e-181 Length: 1212
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x US-09-620-312D-687 (1-1212)
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QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAala 20
Db 131 ATGACGGAAACAGGCGCATCTCTTCCCAAGACTTCTTGGCCGAGGAGCATCGCCGCCGCC 190
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuLeuGlnValGlnHis 40
Db 191 ATCTCCAGAGCGCGCTGGCTCCGATCGAGCGGTCAGGCTGCTGCTGAGTCCAGCAC 250
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 251 GCCAGCAAGCAGATCGCCGCCGACAGCAGTACAAGGGCATCGTGGACTGCTGATTCCTG 310
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 311 ATCCCAAGGAGCGGCTGCTCTCTTGGAGGGGCAACCTTGGCAACGTCATTCGC 370
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 371 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAAGTACAAGCAGATCTTCTCTG 430
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 431 GGGGGCGTGGACAGACACAGCTTCTGAGGTACTTTCGGGCAACCTGGGCTCCGCC 490
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 491 GGTGGCGCGCGGACCTCTCTCTGCTGTGTACCGCTGGATTTTGCAGAACCCGC 550
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGlnArgGluPheArgGlyLeuGlyAspCys 160
Db 551 CTGCAGCGGAGTGGGAAAGTCAAGCAGAGCGGAGTTCGAGGCTTGGAGAGACTGC 610
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
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APPLICATION NUMBER: US/08/961.871
 FILING DATE: 31-OCT-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/030,017
 FILING DATE: 01-NOV-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferber, Donna M.
 REGISTRATION NUMBER: 33,878
 REFERENCE/DOCKET NUMBER: 78-96
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 499-8080
 TELEFAX: (303) 499-8089
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1177 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: not relevant
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 94...990
 US-08-961-871-9

Alignment Scores:
 Pred. No.: 2,3e-165 Length: 1177
 Score: 1412.00 Matches: 264
 Percent Similarity: 94.97% Conservative: 19
 Best Local Similarity: 88.59% Mismatches: 15
 Query Match: 91.51% Indels: 0
 DB: 3 Gaps: 0

US-09-811-094-33 (1-298) x US-08-961-871-9 (1-1177)

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QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAala 20
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QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 154 GTCTCCAGACCGCGTCCGCCCGATCGAGAGGTCAAACTGCTGCTGCGAGTCCAGCAT 213
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 214 GCCAGCAACAGATCAGTGCAGAGAAGCAGTACAAAGGCATCATGATTGTCGTGAGA 273
QY 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyValAsnLeuAlaValIleArg 80
DB 274 ATCCCAAGAGCAGCGCTTCTCTCTTTCTGGAGGGGTAACTGGCCACGATGATCCGG 333
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 334 TACTTCCCACTCAAGCCCTGAATCTCGCTTCAAGACAGTACAGCAGATCTTCTCTG 393
QY 101 GlyGlyValAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 394 GGAGCGGTGTATCGACATAGCAGTCTTCTGCGCTACTTCTGCTGAACCTGGCTCTGGT 453
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
DB 454 GGGGCGAGTGGGGCCACTCTCTGCTTCTGCTACCGCTGGACTTGTCTAGGACCCAG 513
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 514 CTGGCTCGGACGCGGGCAAGGGATCTCCACGAGAAATCAATGGCTGGCGCACTGT 573
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 574 CTCACCAAGATCTTCAAGTCGGAGCGCTGAGGGTCTCTACCGAGGTTCAGTGTCTCT 633

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QY 181 ValGlnGlyIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 634 GTCCAGGGCATCATCATCTACAGAGCTGCTTCTCGAGTCTATGACACATGCCAAGGG 693
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
DB 694 ATGCTGCCAGACCCCAAGAATGTGCACATTATCGTGAGCTGCGATGATTGCCAGAGTGT 753
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValAlaCysArgMetMetMet 240
DB 754 ACAGCGTTGCGGGCTGTGTCTTATCCGTTTGACACTGTTTCGCTGAGGATGATGATG 813
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
DB 814 CAGTCTGGCCGCAAGAGGCTGATATTATGTACACGGGACACTTGTGCTGGAGGAAG 873
QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
DB 874 ATTGCAAAAGATGAAGAGCCCAACGCTTCTTCAAAGGTGCTTGTGCTCAATGTACTGAGA 933
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
DB 934 GGCATGGGTGCTGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 987

```

RESULT 5

US-09-566-921-66
 ; Sequence 66, Application US/09566921
 ; Patent No. 6682888
 ; GENERAL INFORMATION:
 ; APPLICANT: Loring, Jeanne F.
 ; APPLICANT: Tingley, Debra W.
 ; APPLICANT: Edwards, Carla M.
 ; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
 ; FILE REFERENCE: PA-0024 US
 ; CURRENT APPLICATION NUMBER: US/09/566,921
 ; CURRENT FILING DATE: 2000-05-05
 ; NUMBER OF SEQ ID NOS: 138
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 66
 ; LENGTH: 1747
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. 6682888 244561.6
 US-09-566-921-66

Alignment Scores:
 Pred. No.: 9,79e-165 Length: 1747
 Score: 1409.00 Matches: 263
 Percent Similarity: 94.63% Conservative: 19
 Best Local Similarity: 88.26% Mismatches: 16
 Query Match: 91.32% Indels: 0
 DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x US-09-566-921-66 (1-1747)

```

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAala 20
DB 126 ATGGGTGATCAGGTTGAGCTTCTTAAGGACTTCTTGGCGGGGCGTGGCGCTGCC 185
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 186 GTCTCCAGACCGCGTCCGCCCATCGAGAGGTCAAACTGCTGCTGCGAGTCCAGCAT 245
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 246 GCCAGCAACAGATCAGTGTGAGAGCAGTACAAAGGGATCAATTGATTGTGTGTGAGA 305
QY 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
DB 306 ATCCCAAGAGCAGGCTTCTCTCTTCTGGAGGGGTAACTGCGCAACGTCATCTCGT 365

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QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnPheLeu 100
Db TACTTCCCAACCAAGCTCTCACTTCGCTTCAAGGACAGTACAGGAGCTCTTTA 425
QY 101 GlyGlyValAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db GGGGTGTGGATGGGATCAAGCAGTTCTGGGCTACTTTGTGTGTAACCTGGCTCCGGT 485
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db GGGGCGCTGGGCGCACCTTCCTTTGCTTACCGCTGGACTTGTGTAGACCAAG 545
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db TTGGCTGTGTATGGGCAAGGGCGCCCGCCAGCGTCAAGTTCCTGGGCGACTGT 605
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db ATCATCAAGATCTTCAAGTCTGATGGCTGAGGGGGCTCTACCAAGGGTTTCAAGCTCT 665
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db GTCCAAAGCATATTATATAGAGTGCCTACTTCGGAGTCTATGATCTGCGCAAGGG 725
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db ATGCTGCTGATGCCCAAGAGCGGATTTTGTGAGCTGGATGATTGCGCCAGAGTGT 785
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db ACGGAGTTCGAGGGCTGTCTCTACCCCTTGCACACTGTTCGTGTAGATGATG 845
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db CAGTCCGCGCGGAAAGGGCGGATATTATGATACACGGGACAGTTGACTGTGCGAGGAA 905
QY 261 IlePheArgAspGluGlyGlyValAlaPheLysGlyAlaTrpSerAsnValIleArg 280
Db ATTCAAGAGCAGAGGAGCGGCTTCTCAAGGTGCTGTGTGCTCAATGTCTGAGA 965
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
Db GGATGCGCGTGTCTTTGTATTGTGTGTATGATGATGATCAAAAAATATGTC 1019

RESULT 6

US-08-961-871-11
; Sequence 11, Application US/08961871
; Patent No. 6013858
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; APPLICANT: Graham, Brett H.
; APPLICANT: MacGregor, Grant R.
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
; TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GreenLee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961.871
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 190..1086
US-08-961-871-11
Alignment Scores:
Pred. No.: 1-87e-164 Length: 1259
Score: 1405.00 Matches: 263
Percent Similarity: 94.30% Conservative: 18
Best Local Similarity: 88.26% Mismatches: 17
Query Match: 91.06% Indels: 0
DB: 3 Gaps: 0

US-09-811-094-33 (1-298) x US-08-961-871-11 (1-1259)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
Db 190 ATGGGGGATCAGCTTTTGTAGCTTTCTTAAGGACTTCTCTGGCAGGTGGCATCCCGCGCC 249
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 250 GTCTCCAAAGCGCGTCCCGGATCGAGAGGTCCTCAAGGCTCAATCTGCTGCGAGTCCAGCAT 309
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 310 GCCAGCAACAGATCAGTCAGAGAGAGAGTACAAAGGCTCATTTGTTGCTGCTGAGA 369
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 370 ATCCCAAGGAGCAGGCTTCTCTCTTCTGGAGGGGTAACTGGCCCAACGTGATCCGG 429
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 430 TACTTCCCACTCAAGCCCTGAACCTTCGCTTCAAGACACAGTACAAAGCAGATCTTCCTG 489
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 490 GGAGGGGTGGATGCCATAAGCAGTTCTGGCGCTACTTTGCTGGTAACCTGGCTCTGCT 549
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 550 GGGGAGCTGGGGCACCTCCCTCTGCTCTACCCGCTGAGCTTGTCTAGGACCAAG 609
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 610 CTGGCTGCCGACGTGGGCAAGGATCTTCCAGCAGAGATTCATATGGGCTGGCGCACTGT 669
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 670 CTCACCAAGATCTTCAAGTCGAGCGGCTGACGGGTCTCTACCAAGGTTCAGTGTCTCT 729
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 730 GTCCAGGGCATCATCATCTACAGAGCTGCTACTTCGGAGTCTATGACACTGCCAAGGG 789
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220

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Db      790 ATGCTGCCAGACCCCAAGATGTCACATTATCTGTGAGCTGGATGATGCCAGAGTGTG 849
Qy      221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgAspMetMetMet 240
Db      850 ACAAGGTGGGGGGCTGGTGTCTATCCGTTTGACACTGCTGCTGAGATGATGATG 909
Qy      241 GlnSerGlyArgLysGlyAlaAspIleValMetTyrThrGlyThrValAspCysTyrArgLys 260
Db      910 CAGTCTGCCCGCAAGGGCTGATATTATGTATACACGGGGACACTTACTGCTGGAGGAG 969
Qy      261 IlePheArgAspGluGlyGlyAlaPhePhePheLysGlyAlaTyrSerAsnValLeuArg 280
Db      970 ATTGCMAAAGATGAGAGGACCAACGCTTTCTTCAAGGTGCTGGTCCAAATGACTGAGA 1029
Qy      281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
Db      1030 GGCATGGGTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1083

RESULT 7
US-09-434-354-1
; Sequence 1, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Cleverger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andrejev, Alexander Y.
; APPLICANT: Frigeri, Luciano G.
; APPLICANT: Velicelbi, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-434-354-1

Alignment Scores:
Pred. No.: 2,93e-162 Length: 894
Score: 1385.50 Matches: 260
Percent Similarity: 94.30% Conservative: 21
Best Local Similarity: 87.25% Mismatches: 16
Query Match: 89.79% Indels: 1
DB: 4 Gaps: 1

US-09-811-094-33 (1-298) x US-09-434-354-1 (1-894)
Qy      1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAlaAla 20
Db      1 ATGGGTGATCATCGCTTGGAGTCTCTAAAGGACTTCTGCGCGGGCGGTGCGCGTGC 60
Qy      21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db      61 GTCTCCAGACGGCGGTGCGCGCCCATCGAGAGGTCAAACTGCTGCGAGGTCCAGCAT 120
Qy      41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db      121 GCCAGCAACACAGTACAGTGTGAGACAGTACAAAGGATCATTCATTGTTGGTGCAGA 180
Qy      61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaValIleArg 80
Db      181 ATCCCTAAGGAGGAGGGCTTCTCTCTCTGAGGGGGTAACTGGCCAAACGTGATCCGT 240
Qy      81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100

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Db      241 TACTTCCCCACCCCAAGCTCTCAACTTCGCCCTTCAAGGCAAGTACAGCAGCTCTTCTTA 300
Qy      101 GlyGlyValAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db      301 GGGGGTGGTGGATCGGCATAGCAGTTCTGGCGCTACTTTTGGTAACTGGCGTCCGGT 360
Qy      121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaThrArg 140
Db      361 GGGGGCGTGGGGCCACCTCCCTTTGCTTGTACCCGCTGGACTTTTCTAGGACACAGG 420
Qy      141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db      421 TTGGGTGCTGATGGGCGAGGCGC---GCCCAGCGTGAAGTCCATGCTGCTGGCGACTGT 477
Qy      161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db      478 ATCATCAAGATCTTCACAGTCTGATGGCCTGAGGGGCTCTACAGGGTTTCAACGCTCT 537
Qy      181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db      538 GTCCAGAGCATCATTCATCTAGAGTCCCTACTTCGGAGTCTATGATGATGCTCCAGGGG 597
Qy      201 MetLeuProAspProLysAsnThrHisIleValValSerTyrMetIleAlaGlnThrVal 220
Db      598 ATGCTGCTGACCCCAAGAGCGTGACATTTTGTGAGCTGCATGATGCTCCAGAGTGTG 657
Qy      221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgAspMetMetMet 240
Db      658 ACGGCGTGGAGGGCTGCTGCTTACCCCTTTGACACTGTTCTGCTAGATGATGATG 717
Qy      241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260
Db      718 CAGTCCGCGCGAAAGGGCGCATATTATGTACACGGGGACAGTTGACTGCTGGAGGAG 777
Qy      261 IlePheArgAspGluGlyGlyAlaPhePheLysGlyAlaTyrSerAsnValLeuArg 280
Db      778 ATTGCMAAAGACAGAGGACCAAGCCCTTCTCAAAAGTGCCTGCTGCTCAATGCTGAGA 837
Qy      281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
Db      838 GGCATGGGGGGTGTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 891

RESULT 8
US-09-621-976-810
; Sequence 810, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 810
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 104...388
US-09-621-976-810

Alignment Scores:
Pred. No.: 2,86e-44 Length: 389
Score: 429.50 Matches: 91
Percent Similarity: 98.91% Conservative: 0
Best Local Similarity: 98.91% Mismatches: 1
Query Match: 27.84% Indels: 1
DB: 4 Gaps: 0

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US-09-811-094-33 (1-298) x US-09-621-976-810 (1-389)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
Db 104 ATGACGGAACAGCCATCTCTCGCCAAAGACTTCTTGGCCGGAS--ATCGCCGCGCC 161
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 162 ATCTCCAAAGCGCGTGGCTCGATCGAGCGGTCAGCTGCTGCGAGTCCAGCAC 221
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 222 GCCAGCAAGCAGATCGCCCGCAGCAGTACAGGGCATCGTGGACTGCATTGTCGCG 281
QY 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
Db 282 ATCCCAAGAGCAGCGCGTGTGTCCTTCCTGGAGGGCAACCTTGCACCAAGTCATTGCG 341
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLys 92
Db 342 TACTTCCCMACTCAAGCCCTCAACTTCGCGCTTCAAG 377

RESULT 9

US-09-621-976-608
; Sequence 608, Application US/09621976
; Patent No. 6639063

GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 608

; LENGTH: 383

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 105..383

US-09-621-976-608

Alignment Scores:
Pred. No.: 3,51e-41 Length: 383
Score: 404.50 Matches: 87
Percent Similarity: 94.5% Conservative: 0
Best Local Similarity: 94.5% Mismatches: 5
Query Match: 26.22% Indels: 1
DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x US-09-621-976-608 (1-383)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
Db 105 ATGACGGAACAGCCATCTCTTSCCAAAGACTTCTTGGCCGGAG--ATCGCCGCGCC 162
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 163 ATCTCCAAAGCGCGTGGCTCGATCGAGCGGTCAGCTGCTGCGAGTCCAGCAC 222
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 223 GCCAGCAAGCAGATCGCCCGCAGCAGTACAGGGCATCGTGGACTGCATTGTCGCG 282
QY 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
Db 283 ATCCCAAGAGCAGCGCGTGTGTCCTTCCTGGAGGGCAACCTTGCACCAAGTCATTGCG 342
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLys 92

Db 343 TACTTCCCMACTCAAGCCCTCAASTTGCCTTCAAA 378

RESULT 10

US-09-621-976-610

; Sequence 610, Application US/09621976

; Patent No. 6639063

GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 610

; LENGTH: 416

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 142..414

; NAME/KEY: misc feature

; LOCATION: 150,152,162,172

; OTHER INFORMATION: n=a, g, c or t

US-09-621-976-610

Alignment Scores:

Pred. No.: 1,33e-36 Length: 416
Score: 368.00 Matches: 74
Percent Similarity: 95.18% Conservative: 5
Best Local Similarity: 89.16% Mismatches: 4
Query Match: 23.85% Indels: 1
DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x US-09-621-976-610 (1-416)

QY 116 AsnLeuAlaSerGlyGlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAsp 135
Db 167 ATCTGTCATCGGTGGGCGCCGAGGCC--ACATCCCTGTGTTTGTACCTCTGTAT 225
QY 136 PheAlaArgThrArgLeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArg 155
Db 226 TTTRCCGTACCGCTCTAGCAGCTGATGGGTAAAGCTGGAGCTGAAGGGATTCGA 285
QY 156 GlyLeuGlyAspCysLeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGln 175
Db 286 GGCTCGGTGACTGCTGTGTTAAGATCTACAAATCTGATGGGATTAAGGGCCTGTACCA 345
QY 176 GlyPheSerValSerValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyr 195
Db 346 GGCTTAAACATGTCTGTGAGGGTATTATCACTACCGAGCGCCTACTTCGGTATCTAT 405
QY 196 AspThrAla 198
Db 406 GACACTGCA 414

RESULT 11

US-09-833-381-204/c

; Sequence 204, Application US/09833381

; Patent No. 6672186

GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; CURRENT FILING DATE: 2001-04-11

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 204

```

; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-204

Alignment Scores:
Pred. No.: 1.09e-31 Length: 565
Score: 330.00 Matches: 69
Percent Similarity: 76.72% Conservative: 20
Best Local Similarity: 59.48% Mismatches: 22
Query Match: 21.39% Indels: 5
DB: 4 Gaps: 1

US-09-811-094-33 (1-298) x US-09-833-381-204 (1-565)
QY 184 IleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGlyMetLeuPro 203
Db 565 ATCATGTGTACCGAGCCCTCTTTTGGAGCTTATGACAGTTACACAGTTAAGGGTTATTACCA 506
QY 204 AspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThr--ValThrAlaV 223
Db 505 AAGCCACAGAAACCCATTCTTGTCTCTCTTTTTCATTGCTCAAGTTGAGTACTACAT 446
QY 223 alAlaGlyValValSerTyrProPheAspThrValArgArgMetMetGlnSerG 243
Db 445 GCTCTGGAACTCTTCTTATCCCTTTTGACAGTTAGAACGCTATGATGACGAGTG 386
QY 243 lYArgLysGlyAlaAspIleMetTyrThrGlyThr--ValAspCysTrpArgLysIlePhe 262
Db 385 GTGAG-----GCTAACGGCAATATAAAGAACCTTTAGACTGCTTTGTGAAGATATAC 332
QY 263 ArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArgGlyMet 282
Db 331 CAACATGAAGGAATCAGTTCCTTTTTCGTGGCGCTTCTCCAAATGTTCTTCGGGGTACA 272
QY 283 GlyGlyAlaPheValLeuValLeuTyrAspGlyLeuLysLys 296
Db 271 GGGGGTGTCTGGTGTGTATATATATGATAAATAAAGAA 230

RESULT 12
US-09-188-930-262
; Sequence 262, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 262
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Mouse
US-09-188-930-262

Alignment Scores:
Pred. No.: 1.43e-28 Length: 1816
Score: 311.00 Matches: 88
Percent Similarity: 50.17% Conservative: 62
Best Local Similarity: 29.43% Mismatches: 111
Query Match: 20.16% Indels: 38
DB: 3 Gaps: 11

US-09-811-094-33 (1-298) x US-09-188-930-262 (1-1816)
QY 10 LysAspPheLeuAlaGlyGlyIleAlaAlaIleSerLysThrAlaValaProfile 29

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Db 623 AGGCACCTGGTGGCAGGAGGTGGGCAGGGCAGTTTCCAGAACCTGCACTGCCCCCTGTG 682
QY 30 GluArgValLysLeuLeuGlnHisAlaSerLysGlnIleAlaAlaAspLys 49
Db 683 GACAGACTGAGGTGCTCATGCAGGTC---CATGCTCCCGC-----AGC 724
QY 50 GlnTyrLysGlyIleValAspCysIleValArgIleProLysGluGlnGlyValLeuSer 69
Db 725 AACAAACATGTCATCTAGTGGATTACACAGATGATTTCGAGAGGGGGAGCCCAAGTCA 784
QY 70 PheTrpArgGlyAsnLeuAlaAsnValIleArgTyrPheProThrGlnAlaLeuAsnPhe 89
Db 785 CTCTGGGGGGCAACGGCATCATGTCTCTCAAAATTGCCCTGAGTCGCCCATCAATTC 844
QY 90 AlaPheLysAspLysTyrLysGlnIlePheLeuGlyValAspLysGlyHisThrGlnPhe 109
Db 845 ATGGCATATGACAGATGAACGG-----CTTGTGGTAGTGTATCAGGAGACG----- 892
QY 110 TrpArgTyrPheAlaGlyAsnLeuAlaSerGlyGlyAlaAlaGlyAlaThrSerLeuCys 129
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QY 130 PheValTyrProLeuAspPheAlaArgThrArgLeuAlaAlaAspValGlyLysSerGly 149
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QY 150 ThrGluArgGluPheArgGlyLeuGlyAspCysLeuValLysIleThrLysSerAspGly 169
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QY 170 IleArgGlyLeuTyrGlnGlyPheSerValSerValGlnGlyIleIleIleIleIleArgAla 189
Db 1055 GTAGTGCTCTTACAAAGGTACATCCCCACATGCTGGGATCATCCCTATGCTGCTG 1114
QY 190 AlaTyrPheGlyValTyrAspThrAlaLysGlyMetLeuProAspProLysAsnThrHis 209
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QY 210 Ile-----ValValSerTrpMetIleAlaGln 218
Db 1154 CTCCAGCGCTACGAGTAACAGTGCAGACCCCGGTGTGCTGCTCTGCGCTGTGTGT 1213
QY 219 ThrValThrAlaValAlaGly---ValValSerTyrProPheAspThrValArgArg 237
Db 1214 ACTATCTCCAGTACTTGTGGCCAGCTGGCCAGCTACCCACACTAGCCCTGTGTCAGGACCCGG 1273
QY 238 MetMetGlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCys 257
Db 1274 ATGACGGCACAAAGCCTCCATTGAGGGCGCACCTGAGGTAAACCATGAGCAGCCCTC----- 1327
QY 258 TrpArgLysIlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsn 277
Db 1328 TTCAACACATCTCGGACTGAGGGGCTTTGGGCTCTACCGGGGCTGCCCCCAAC 1387
QY 278 ValLeuArgGlyMetGlyAlaPheVal---LeuValLeuTyrAspGlnLeuLys 295
Db 1388 TTTCATGAAGGTGATCCCGCTGTGAGCATCAGTACGTGTCTACGAAACCTGAAG 1444

RESULT 13
US-09-312-283C-262
; Sequence 262, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c2

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[illegible]

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Db 1324 GAAAGGCCATAACTGACTGTTAATGATTTTTCGGGACAAATTTACCAAGAGAT 1383
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 1384 GCCTCTGTCCA-----CTTCAGCAGAGAATTTCTGTGGA 1419
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 1420 GCCTGTCTGGAGGCTCTCAGGCTCATTTTACCAACCATTTGGAGTAGTGAAGATCGT 1479
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
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QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 1528 -----AATGTCTCCGGGACTTGGGAATTTTGTCTGTATAGGGTGCACAGCGGT 1581
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QY 237 ArgMetMetGlnSerGlyArgGlyAlaAlaAspIleMetTyrThrGlyThrValAsp 256
Db 1753 AGA-----CTGCAGGTGGCTGCCGGCTGCGCCAGACGACATACAGTGTGTCTATCGAC 1806
QY 257 CysTrpArgLysIlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSer 276
Db 1807 TGTTCAGGAAGATTCTCCGGGAAGAGAGGGCCCTCAGCATTTTGGAAAGGAGCTGCAGCT 1866
QY 277 AsnValLeuArgGlyMetGlyGly---AlaPheValLeuValLeuTyrAspGluLeuLys 295
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QY 296 Lys 296
Db 1927 CGG 1929

RESULT 15

US-09-016-434-622
; Sequence 622, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 622:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LIVRUT04
; CLONE: 2517151
US-09-016-434-622
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Best Local Similarity: 98.48% Mismatches: 1
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Job time : 133 secs

GenCore version 5.1.6
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Run on: August 17, 2004, 19:33:59 ; Search time 530 Seconds
(without alignments)
2758.810 Million cell updates/sec

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Perfect score: 1543

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Searched: 3225727 seqs, 2453303834 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 4: /cg2_6/ptodata/2/pubpna/US06_PUBCOMB.seq*
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- 10: /cg2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq*
- 11: /cg2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq*
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- 14: /cg2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq*
- 15: /cg2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq*
- 16: /cg2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq*
- 17: /cg2_6/ptodata/2/pubpna/US10_NEW_PUB.seq*
- 18: /cg2_6/ptodata/2/pubpna/US60_NEW_PUB.seq*
- 19: /cg2_6/ptodata/2/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	1543	100.0	897	9	US-09-810-644-3	Sequence 3, Appli
3	1543	100.0	897	9	US-09-185-904A-3	Sequence 3, Appli
4	1543	100.0	1212	15	US-10-037-270-687	Sequence 687, App
5	1543	100.0	1212	16	US-10-117-722-687	Sequence 687, App
6	1510	97.9	2592	14	US-10-044-090-152	Sequence 152, App
7	1463	94.8	1385	16	US-10-062-674-1973	Sequence 1973, Ap
8	1454	94.2	897	9	US-09-811-094-2	Sequence 2, Appli
9	1454	94.2	897	9	US-09-810-644-2	Sequence 2, Appli
10	1454	94.2	897	9	US-09-185-904A-2	Sequence 2, Appli
11	1454	94.2	1228	16	US-10-116-275-301	Sequence 301, App
12	1451	94.0	1215	16	US-10-191-803-135	Sequence 1135, Ap
13	1446	93.7	1243	13	US-10-403-571-153	Sequence 153, App
14	1424	92.3	1196	9	US-09-917-800A-1327	Sequence 1327, Ap
15	1409	91.3	1711	15	US-10-198-846-13437	Sequence 13437, A
16	1385.5	89.8	894	9	US-09-811-094-1	Sequence 1, Appli
17	1385.5	89.8	894	9	US-09-810-644-1	Sequence 1, Appli
18	1385.5	89.8	894	9	US-09-185-904A-1	Sequence 1, Appli
19	1385.5	89.8	1320	10	US-09-738-630-70	Sequence 70, Appl
20	1356.5	87.9	1116	9	US-09-969-708-213	Sequence 213, App
21	1356.5	87.9	1116	9	US-09-880-107-2096	Sequence 2096, Ap
22	1356.5	87.9	1116	15	US-10-171-581-48	Sequence 48, Appl
23	1193	77.3	2706	15	US-10-103-313-611	Sequence 611, Appl
24	1193	77.3	2706	16	US-10-158-034-121	Sequence 121, App
25	1184.5	76.8	925	16	US-10-161-927-5	Sequence 5, Appli
26	1081	70.1	687	16	US-10-264-049-2162	Sequence 2162, Ap
27	1021.5	66.2	977	16	US-10-369-493-29759	Sequence 29759, A
28	1003	65.0	976	16	US-10-369-493-28790	Sequence 28790, A
29	993.5	64.4	903	16	US-10-369-493-28775	Sequence 28775, A
30	979.5	63.5	5768	10	US-09-873-367C-134	Sequence 134, App
31	936	60.7	720	9	US-09-910-943-105	Sequence 105, Appl
32	840	54.4	639	17	US-10-404-460-10	Sequence 10, Appl
33	811	52.6	537	13	US-10-029-386-20882	Sequence 20882, A
34	809.5	52.5	612	13	US-10-424-599-50040	Sequence 50040, A
35	796	51.6	943	12	US-09-876-143-1254	Sequence 1254, Ap
36	793.5	51.4	543	13	US-10-621-901-2291	Sequence 2291, Ap
37	788.5	51.1	906	15	US-10-032-585-6194	Sequence 6194, Ap
38	778.5	50.5	924	16	US-10-369-493-25137	Sequence 25137, A
39	769	49.8	966	16	US-10-369-493-25061	Sequence 25061, A
40	760.5	49.3	954	16	US-10-369-493-25108	Sequence 25108, A
41	760.5	49.3	957	9	US-09-801-368-251	Sequence 251, App
42	754.5	48.9	933	16	US-10-320-797-2092	Sequence 2092, Ap
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44	751.5	48.7	1593	13	US-10-424-599-25174	Sequence 25174, A
45	751	48.7	1523	13	US-10-425-114-26646	Sequence 26646, A

ALIGNMENTS

RESULT 1

US-09-811-094-33
; Sequence 3, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Cleveenger, William
; APPLICANT: Wiley, Sandra Bileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yashong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 897

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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-811-094-33

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DB 181 ATCCCCAAGGACGAGCGGTGCTGCTCTTCTGGAGGGCAACCTTGCCAACTGCTTCGC 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
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Qy	81	TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu	100
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Qy	101	GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly	120
Db	301	GGGGCGGTGGCAAGCACACGCAGTTCCTGGAGGTACTTTCGGGCACACCTGGGCTCCGGC	360
Qy	121	GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg	140
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Qy	141	LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys	160
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Db	481	CTGGTGAAGATCCCAAGTCCGACGGCATCCGGGCGCTTACCAGGGCTTCAGTGTCCTC	540
Qy	181	ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly	200
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Qy	221	ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet	240
Db	661	ACGGCGGTGGCGGGGTGGTGTCCTACCCCTTCGACACGGTGGCGGCGCATGATGATG	720
Qy	241	GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys	260
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US-09-185-904A-3

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RESULT 4
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; Sequence 687, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: NO. US20030104529
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B

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; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 687
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (131)..(1027)
US-10-037-270-687

Alignment Scores:
Pred. No.: 2,66e-202 Length: 1212
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-811-094-33 (1-298) x US-10-037-270-687 (1-1212)
QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
DB 131 ATGACGGAACAGCCATCTCTTCGCAAGACATCTTTGGCGGAGCATCGCGCGCC 190
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuGlnValGlnHis 40
DB 191 ATCTCCAAAGACGGCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGAGTCCAG 250
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnIleValAlaAspCysIleValArg 60
DB 251 GCCAGCAACAGCATCGCGCCACAGCAGTACAAGGCGATCGTGGACTGCTTCGCG 310
QY 61 IleProLysGluGlnGlyValLeuSerPheThrArgGlyValLeuAlaAsnValIleArg 80
DB 311 ATCCCAAGAGCAGGGCGTCTCTTCCTTCGAGGGGCAACCTTGCCAAAGCTCATTCGC 370
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 371 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAGTACAAGCAGATCTTCCTG 430
QY 101 GlyGlyValAspLysHisThrGlnPheThrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 431 GGGGCGTGGACAGCAGCAGTCTCGAGGTACTTTGGGGCAACCTGGCGCTCCGGC 490
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaAspThrArg 140
DB 491 GGTGCGCGCGCGCACCTCTCTGCTGTGTACCCGCTGGATTCGCCAGAACCCGC 550
QY 141 LeuAlaAlaAspValCysLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 551 CTGGCAGCGGACGTGGGAAGTCAAGCAGCAGCGCGAGTTCGAGGCTGGGAGACTGC 610
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 611 CTGGTGAAGATCACCAGTCCGACGGCATCGGGGCTGTACCAAGGCTTCAGTGTCTCC 670
QY 181 ValGlnGlyIleIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 671 GTGCAGGCGATCATCATCTACCGCGCGCTACTTCGCGGTGTACGATACGCCCAAGGC 730
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
DB 731 ATGCTCCCGACCCCAAGAACACGACATCGTGTGTGAGCTGGATGATGCGCAGACCGTG 790
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgAtgMetMetMet 240
DB 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 851 CAGTCCGCGCGCAAGAGGAGCTGACATCATGTACACGGCACCGTCCGACTGTGTGAGGAAG 910
QY 261 IlePheArgAspGluGlyGlyIleAlaPhePheLysGlyAlaTyrSerAsnValLeuArg 280
DB 911 ATCTTTCAGAGATGAGGGGGCAAGCCCTTCTCAAGGGTGGTGGTCCCAAGCTCCTCGG 970
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
DB 971 GGCATGGGGGGCGCTTCTGCTGCTGTGACGAGAGCTCAAGAAGGTGATC 1024

RESULT 5
US-10-117-722-687
; Sequence 687, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
; TITLE OF INVENTION: Polydeptides
; FILE REFERENCE: 784CIP2BCIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 687
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (131)..(1027)
US-10-117-722-687

Alignment Scores:
Pred. No.: 2,66e-202 Length: 1212
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-811-094-33 (1-298) x US-10-117-722-687 (1-1212)
QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
DB 131 ATGACGGAACAGCCATCTCTTCGCAAGACATCTTTGGCGGAGCATCGCGCGCC 190
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuGlnValGlnHis 40
DB 191 ATCTCCAAAGACGGCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGAGTCCAG 250
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnIleValAlaAspCysIleValArg 60
DB 251 GCCAGCAACAGCATCGCGCCACAGCAGTACAAGGCGATCGTGGACTGCTTCGCG 310
QY 61 IleProLysGluGlnGlyValLeuSerPheThrArgGlyValLeuAlaAsnValIleArg 80
DB 311 ATCCCAAGAGCAGGGCGTCTCTTCCTTCGAGGGGCAACCTTGCCAAAGCTCATTCGC 370
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 371 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAGTACAAGCAGATCTTCCTG 430
QY 101 GlyGlyValAspLysHisThrGlnPheThrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 431 GGGGCGTGGACAGCAGCAGTCTCGAGGTACTTTGGGGCAACCTGGCGCTCCGGC 490
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaAspThrArg 140
DB 491 GGTGCGCGCGCGCACCTCTCTGCTGTGTACCCGCTGGATTCGCCAGAACCCGC 550
QY 141 LeuAlaAlaAspValCysLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 551 CTGGCAGCGGACGTGGGAAGTCAAGCAGCAGCGCGAGTTCGAGGCTGGGAGACTGC 610
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 611 CTGGTGAAGATCACCAGTCCGACGGCATCGGGGCTGTACCAAGGCTTCAGTGTCTCC 670
QY 181 ValGlnGlyIleIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 671 GTGCAGGCGATCATCATCTACCGCGCGCTACTTCGCGGTGTACGATACGCCCAAGGC 730
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
DB 731 ATGCTCCCGACCCCAAGAACACGACATCGTGTGTGAGCTGGATGATGCGCAGACCGTG 790
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgAtgMetMetMet 240
DB 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
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Db 371 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAGTACAGGAGATCTTCCTG 430
Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 431 GGGGGCGTGGGACAAAGCACACACAGTTCCTGGAGGTACTTTGGGGCAACCTGGCCCTCGGC 490
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaAaTgThrArg 140
Db 491 GGTGGGGCGGGGAGCCCTCCTCTGTCTTGTGTACCCGCTGGATTTCCGACAGAACCCGC 550
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 551 CTGGCAGCGGACGTGGGAAAGTCAAGGCACACAGCGCGAGTTCCGAGGCGCTGGGAGACTGC 610
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 611 CTGTGAAGATCACCAAGTCCGACGGCATCCGGGGCTGTACCGAGGCTTCAGTGTCTCC 670
Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 671 GTGCAGGGCATCATCATCTACCGGGCGCTTCTTGGCGTGTACGATACGGCCAGGGC 730
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 731 ATGCTCCCGACCCCAAGAACACACACATCTGTGTGAGCTGGATGATCGCGACACCGTG 790
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 791 ACGGCGTGGCGGGGTGTCTTACCCCTTCACACCGTGGCGGGCGGCGATGATG 850
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 851 CAGTCCGGCGCAAGAGAGTGCATCATGTATACACGGCACCGTGCAGTGTGGGAAG 910
Qy 261 IlePheArgAspGluGlyGlyValAlaPhePheLysGlyAlaTrpSerAsnValIleArg 280
Db 911 ATCTTCAGAGATGAGGGGGGAGGCCCTTCTCAAGGTGCTGTGTCAACGCTCTCGCG 970
Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
Db 971 GGCATGGGGGCGCCTTCGTCTGTCTGTCTGTACGACGAGCTCAAGAGGTGATC 1024

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RESULT 6

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US-10-044-090-152
; Sequence 152, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; CURRENT APPLICATION NUMBER: US/10/044,090
; FILE REFERENCE: PA-0028 US
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 152
; LENGTH: 2592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1330214.11
; NAME/KEY: unsure
; LOCATION: 1131..1929
; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-152

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Alignment Scores:

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Pred. No.: 3,09e-197 Length: 2592
Score: 1510.00 Matches: 296
Percent Similarity: 99.33% Conservative: 2
Best Local Similarity: 99.67% Mismatches: 0
Query Match: 97.86% Indels: 2

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Db 14 Gaps: 0
US-09-811-094-33 (1-298) x US-10-044-090-152 (1-2592)
Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIle-AlaAlaAl 20
Db 207 ATGACGGAAACAGGCCATCTCTTCGCCAAAGACTTCTTTGGCCGGAGGACATGGCCGCCGC 266
Qy 20 aIleSerLysThrAlaValAlaProIleGluArg-ValLysLeuLeuLeuGlnValGlnH 40
Db 267 CATCTCCAGACGGCGCTGGCTCCGATCAGCGGGGTCAAGCTGCTGCTGCAGGTCCAGC 326
Qy 40 iSaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValAla 60
Db 327 ACGCCAGCAAGCAGATCGCCGCCGCAAGCGGCTACAAGGGCATCGTGGACTGCATTGTCC 386
Qy 60 rGileProLysGlnGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleAla 80
Db 387 GCATCCCCAAGAGCAGGCGGTGTCTCTTGGAGGGGCAACCTTGGCAACGTATTTC 446
Qy 80 rGtyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheL 100
Db 447 GCTACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAGTACAAGCAGATCTTCC 506
Qy 100 euGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerG 120
Db 507 TGGGGGGCGGTGACAAAGCACACGAGTCTTCTGGAGGTACTTTGCGGGCAACCTGGCCCTCG 566
Qy 120 lyGlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaAaTgThrA 140
Db 567 GCGTGGCGGGCGGGCGGACTCTCCCTGTGTGTGTACCCGCTGGATTTTGCAGNACCC 626
Qy 140 rGleuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspC 160
Db 627 GCCTGGCAGCGGACGTGGGAAAGTACAGGCACAGAGCGCGAGTTCGAGGCTTGGGAGACT 686
Qy 160 ySleuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValS 180
Db 687 GCTGTGTGAAGATCACCAAGTCCGAGCGCATCCGGGGCTGTACCAAGGCTTCAGTGTCT 746
Qy 180 erValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysG 200
Db 747 CCGTGCAGGGCATCATCATCTACCGGGCGCTTCTTCGCGGTGTACGATACGGCCAAAG 806
Qy 200 lyMetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrV 220
Db 807 GCATGTCTCCCGACCCCAAGAACACACACATCATGTGTGTGAGCTGCGATGATCGCGCAGAC 866
Qy 220 alThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetM 240
Db 867 TGAAGCGCGTGGCCGGCGTGGTGTCTTACCCCTTCGACACCGTGGCGGGCGCATGATGA 926
Qy 240 etGlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgL 260
Db 927 TGCAGTCCGGCGCAAGAGAGTGCATCATGTACACGGGCAACCGTGCAGTGTGGAGGA 986
Qy 260 ySlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuA 280
Db 987 AGATCTTCAGAGATGAGGGGGGCAAGGCCCTTCTTCAAGGTGCGGTGCTCAACGCTCTGC 1046
Qy 280 rGglyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
Db 1047 GGGGCATGGGGGCGGCTTCTGTGTCTGTGTACGACGAGCTCAAGAAGGTGATC 1102

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RESULT 7

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US-10-062-674-1973
; Sequence 1973, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674

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; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 1973
; LENGTH: 1385
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 373719.5
US-10-062-674-1973

Alignment Scores:
Pred. No.: 3,61e-191 Length: 1385
Score: 1463.00 Matches: 275
Percent Similarity: 97.30% Conservative: 13
Best Local Similarity: 92.91% Mismatches: 8
Query Match: 94.82% Indels: 0
DB: 16 Gaps: 0

US-09-811-094-33 (1-298) x US-10-062-674-1973 (1-1385)
Qy 1 MetThrGluGlnAlaIleSerPheAlaAspPheLeuAlaGlyIleAlaAlaA 20
Db 116 ATGACAGATGCGGTGTCTTCCCAAGGACTTCTGCGAGGTGAGTGGCGGAGCC 175
Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 176 ATCTCCAGAGCGGCGGAGCCCATCGAGCGGTCAAGCTGCTGCGAGGTGCGAGCAT 235
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTrpLysGlyIleValAspCysIleValArg 60
Db 236 GCCAGCAGCAGATCACTGCAGATAAGCAATACAAAGGCATTATAGACTGCGTGGTCCGT 295
Qy 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 296 ATCTCCAGAGCGGAGGAGTGTCTCTCTGCGCGGTAACTGGCCCAATGTCATCAGA 355
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTrpLysGlnIlePheLeu 100
Db 356 TACTTCCCACCCAGGCTCTTAATCTGCGCTTCAAGATTAATACAGCAGATCTTCTTG 415
Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 416 GGTGGTGTGCACAGAGAACCCAGTTTGTGGCGTACTTTGCAGGGAATCTGGCATCGGT 475
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 476 GGTGCCCGAGGGGCGACATCTCTGTGTTGTGTACCTCTTGAATTTGGCCCGTACCCGT 535
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 536 CTAGCAGCTGATGTGGCTAAAGCTGAGCTGAAAGGGAATTCGAGGCTCGGTGACTGC 595
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 596 CTGTTTAAGATCTCAAAATCTGATGGGATTAAGGCGCTGTACCAAGGCTTTACGTTCT 655
Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 656 GTGCAGGATATATCATCTACCGAGCGCCTACTTCGGTATCTATGACATGCAAGGGA 715
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 716 ATGTTTCCCGATCCCAAGAACCTCATCATGCTCATGAGTGGATGATCGCAGAGCTGTC 775
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 776 ACTGCTGTGGCGGTGACTTCTATCTATTTGACACCGTTCCGCGCGCATGATGATG 835
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260

; 836 CASTCAGGGCGCAAGGAACCTGACATCATGTACACAGCAGCTTGCTGCTGGCGGAG 895
; 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
; 896 ATTGCTCGTGATGAAGAGGCAAGACTTTTTCAGGGTGCATGCTCAATGTTCTCAGA 955
; 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
; 956 GCATGGGTGGTGGCTTTTGTCTTGTATGATGAATCAAGAAG 1003

RESULT 8
US-09-811-094-2
; Sequence 2, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yehong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-811-094-2

Alignment Scores:
Pred. No.: 3,22e-190 Length: 897
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservative: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x US-09-811-094-2 (1-897)
Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAlaA 20
Db 1 ATGACAGATGCGGATGTCTTCCCAAGGACTTCTGCGAGGTGAGTGGCGGAGCC 60
Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 61 ATCTCCAGAGCGGCGGTAGCGCCCATCGAGCGGTCAAGCTGCTGCTGCGAGGTGCGAGCAT 120
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTrpLysGlyIleValAspCysIleValArg 60
Db 121 GCCAGCAGCAGATCACTGCAGATAAGCAATACAAAGGCATTATAGACTGCGTGGTCCGT 180
Qy 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 181 ATCTCCAGAGCAGGAGGATTTCTCTCTTCTGCGCGGTAACTGGCCCAATGTCATCAGA 240
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTrpLysGlnIlePheLeu 100
Db 241 TACTTCCCACCCAGGCTCTTAATCTGCGCTTCAAGATTAATACAGCAGATCTTCTTG 300
Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 301 GGTGGTGTGCACAGAGAGAACCCAGTTTGTGGCGTACTTTTCAGGGAATCTGGCATCGGT 360
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
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Db 361 GTGCGCGAGGCGCACATCCCTGTGTTTGTGTACCCCTCTTGATTTTGCOCGTACCCGT 420
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 421 CTAGCAGCTGATGTGGTAAAGCTGGAGCTGAAAGGAATTCGAGGCGCTCGGTGACTGC 480
Qy 161 LeuValLysIleThrLysSerAspGlyLeuArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 481 CTGGTTAAGATCTCAAAATCTCATGGGATTAAAGGCGCTGTACCAAGGCTTTAAAGCTGTCT 540
Qy 181 ValGlnGlyIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 541 GTGCGAGGTATTATCATCTACCGAGCGCCCTACTTCGGTACTATGACACTGCAAGGGA 600
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 601 ATGCTTCGGGATCCCAAGAACTACATCGTATCATGATGATGATGATGATGATGATG 660
Qy 221 ThrAlaValAlaGlyValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 661 ACTGCTGTGCGGGTGAATCTCCATTCATTTGACCGTTCGCGCGCGCATGATGATG 720
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAlaAspCysTrpArgLys 260
Db 721 CAGTCAGGCGCAAGAACTGACATCATGTACACAGGACGCTTGACTGCTGCGGGAAG 780
Qy 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
Db 781 ATTGCTCGTGATGAAGAGGAAAGCTTTTTCAGAGGCTGATGATGATGATGATGATG 840
Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
Db 841 GGCATGGTGGTGGCTTTTGTGCTTGTGTATGATGAATCAAGAAG 888

RESULT 9

US-09-810-644-2
; Sequence 2, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yashong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-644-2

Alignment Scores:
Pred. No.: 3,228-190 Length: 897
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservative: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
Gaps: 0

US-09-811-094-33 (1-298) x US-09-810-644-2 (1-897)

Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20

Db 1 ATGACAGATCCGCATTTCTTCGCCAAGGACTTCTTGGCAGGTGGAGTGGCGGAGCC 60
Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 61 ATCTCCAGAGCGGGTAGCGCCATCGAGCGGCTCAAGCTGTCTGTCTGAGGTGCAGCAT 120
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 121 GCCCAAGCAGATCATCTGCAGATAAGCAATACAAAGGCATTATAGACTGCGTGGTCCGT 180
Qy 61 IleProLysGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaValIleArg 80
Db 181 ATTCCCAAGAGCAGGAAGTTCCTCTTTCGCGCGGTAACTGGCCCAATGTCATCAGA 240
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 241 TACTTCCCAACCCAGGCTCTTAACCTTCGCCTTCAAAGATAAATACAAAGCAGATCTTCTTG 300
Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 301 GGTGGTGTGGACAAAGAAACCCAGTTTTCGCGCTACTTTTCAGAGGAATCTGGCATCGGT 360
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgTrpArg 140
Db 361 GGTGGCGCAGGCGCACATCCCTGTGTTTGTGTACCTCTTGATTTTGCOCGTACCCGT 420
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 421 CTAGCAGCTGATGTGGGTAAAGCTGAGAGCTGAAAGGGAATTCGAGGCGCTCGGTGACTGC 480
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 481 CTGGTTAAGATCTCAAAATCTGATGGGNTAAGGGCTGTACCAAGGCTTTTACGTTCT 540
Qy 181 ValGlnGlyIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 541 GTGCGAGGTATTATCATCTACCGAGCGGCTACTTCGGTATCTATGACACTGCAAGGGA 600
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 601 ATGCTTCGGGATCCCAAGAACTACATCGTATCATGATGATGATGATGATGATGATG 660
Qy 221 ThrAlaValAlaGlyValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 661 ACTGCTGTGCGGGTGAATCTCCATTCATTTGACCGTTCGCGCGCATGATGATG 720
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 721 CAGTCAGGCGCAAGGAATGACATCATGTCACAGGACGCTTGACTGCTGCGGGAAG 780
Qy 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
Db 781 ATTGCTCGTGATGAAGAGGCAAGCTTTTTCAGAGGCTGATGATGATGATGATGATG 840
Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
Db 841 GGCATGGTGGTGGCTTTTGTGCTTGTGTATGATGAATCAAGAAG 888

RESULT 10

US-09-185-904A-2
; Sequence 2, Application US/09185904A
; Patent No. US20020177185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS

```
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-185-904A-2

Alignment Scores:
Pred. No.: 3,22e-190 Length: 897
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservativeness: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x US-09-185-904A-2 (1-897)
QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaA 20
DB 1 ATGACAGATGCCGATTTCTTCCGCAAGACCTTCTGGCAGGTGGGCGGACGCC 60
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 61 ATCTCCAAAGACGGCGGTAGCGCCCATCGAGCGGCTCAAGCTGCTGCTGCAGGTGCAGCAT 120
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnIleValAspCysIleValArg 60
DB 121 GCCAGCAAGCAGATCACTGCAGATAAGCAATACAAAGCATATTAGACTGCGTGGTCCGT 180
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
DB 181 ATTCACAGAGGAGGAGGAGTCTTCTCTTGGCGGGTAACCTGGCCCAATGTCATCAGA 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysValLysGlnIlePheLeu 100
DB 241 TACTTCCCGACCCAGGCTCTTAACCTGCGCTTCAAGATAAATACAAAGCAGATCTTCCCTG 300
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgGlyValAsnLeuAlaSerGly 120
DB 301 GGTGGTGTGGACAGAACCCAGTTTGGCGCTACTTTGAGGGATCTGGCATCGGGT 360
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
DB 361 GGTGCCGAGGGGCCACATCCCTGTGTTTGTGTACCTCTTGTATTTGGCCCGTACCCGT 420
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 421 CTAGCAGCTGATGGGTAAAGCTGAGCTGAAGAGGAATTTCCAGGCGCTCGGTACTGC 480
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 481 CTGGTTAAGATCTACAAATCTGATGGGATTAAGGCGCTGTACCAAGGCTTAAAGCTGTCT 540
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaThrPheGlyValTyrAspThrAlaLysGly 200
DB 541 GTGCAGGATATATCATCTACCGAGCGCCCTACTTCGGTATCTATGACATGCAAGAGGGA 600
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
DB 601 ATGCTTCGGATCCCAAGACACCTCACATCTCATAGCTGATGATGCGACAGACTGTC 660
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
DB 661 ACTGTGTGTGGGTGCTTACTTCTATCCATTTGACACCGCTTCGCCCGCCGATGATG 720
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
DB 721 CAGTCAGGGCCCAAGGAACTGACATCATGTATACAGCAGCGCTTACTCTGCGGAG 780

; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-116-275-301
; Sequence 301, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 301
; LENGTH: 1228
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-275-301

Alignment Scores:
Pred. No.: 5,24e-190 Length: 1228
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservativeness: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
DB: 16 Gaps: 0

US-09-811-094-33 (1-298) x US-10-116-275-301 (1-1228)
QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaA 20
DB 70 ATGACAGATGCCGATTTCTTCCGCAAGACCTTCTGGCAGGTGGGCGGACGCC 129
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 130 ATCTCCAAAGACGGCGGTAGCGCCCATCGAGCGGCTCAAGCTGCTGCTGCAGGTGCAGCAT 189
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnIleValAspCysIleValArg 60
DB 190 GCCAGCAAGCAGATCACTGCAGATAAGCAATACAAAGCATATTAGACTGCGTGGTCCGT 249
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
DB 250 ATTCACAGAGGAGGAGGATTTCTGCTTTCGCGCGGTAACTGCGCAATGTCATCAGA 309
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysValLysGlnIlePheLeu 100
DB 310 TACTTCCCGACCCAGGCTCTTAACCTGCGCTTCAAGATAAATACAAAGCATATTGCGCATCGGCT 369
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgGlyPheAlaGlyAsnLeuAlaSerGly 120
DB 370 GGTGGTGTGGACAGAACGCCAGTTTGGCGCTACTTTGAGGGAAATCTGCGCATCGGCT 429
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
DB 430 GGTGCCGAGGGGCCACATCCCTGTGTTTGTGTACCTCTTGTATTTGGCCCGTACCCGT 489
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
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490 CTAGCAGCTGATGTGGTAAAGCTGGAGCTGAAAGGAATTCGAGGCTCGGTGACTGC 549
161 LeuVallylsleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
550 CTGGTTAAGATCTACAAATCTGATGGGATTAAAGGCTGTGTACCAAGGCTTTTAAACGTGTCT 609
181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
610 GTGCAGGGAATATCATCTACCGAGCGCTTCTCGTATCTATGACACTGCAAGGGA 669
201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
670 ATGCTTCGGGATCCCAAGAACAACACTCACATCGTCATCAGCTGGATGATCGCACAGCTGTC 729
221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
730 ACTGCTGTGTGGGCTTGAATCTTATCCATTTGACACGTTGCGCGCGCATGATGATG 789
241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
790 CAGTCAGGCGCGCAAGGAACACTGACATCATGTACACAGGCGGCTTGAATGCTGGCGGAAG 849
261 IlePheArgAspGluGlyGlyValAlaPhePheLysGlyAlaTyrSerAsnValLeuArg 280
850 ATGCTCGTGTGATGAAGGAGGCAAGCTTTTTCAGGGTGTGATGATGAATCAAGAAAG 909
281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
910 GCATGGGTGGTGTGCTTTGTGCTTCTGTGATGATGAATCAAGAAAG 957

RESULT 12

US-10-191-803-1135
; Sequence 1135, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 4921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1135
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 D12771
US-10-191-803-1135

Alignment Scores:
Pred. No.: 1,34e-189 Length: 1215
Score: 1451.00 Matches: 272
Percent Similarity: 96.9% Conservative: 15
Best Local Similarity: 91.8% Mismatches: 9
Query Match: 94.0% Indels: 0
DB: 15 Gaps: 0

US-09-811-094-33 (1-298) x US-10-191-803-1135 (1-1215)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
Db 55 ATCAGAGATGCGCTGTGTCCTTCGCCAAGGACTTCTTGGCTGGTGGAGTGGCGGGCC 114
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuLeuGlnValGlnHis 40
Db 115 ATCTCAAGACGCGGTAGCACCATCGAGCGGGTCAAGCTGCTGTCGAGGTGCAGCAC 174
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 175 GCCAGCAGCAATACCGGAGATAGCAATACAGGGCATATAGACTGCGGTGGTTCGT 234
QY 61 IleProLysGlnGlnValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 235 ATCCCAAGGAACAGGAGTCTCTTCTGCGTGGCAACCTGGCCAATGTCTATCAGA 294
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 295 TACTTCCCAACCCAGGCTCTCAACTTTCCTTCAAGATATAATACAGGAGATCTTTTG 354
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 355 GGTGGTGTGGACAAGAGGACCCAGTTTGGCGGTACTTTGCAGGGAACCTGGCATCAGGT 414
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 415 GGTGCTGCTGGGCGCACATCTTGTCTTTGTGTACCTCTTGAATTTGCCCGTACCCGT 474
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 475 CTAGCAGCTGATGTGGCAAGCTGGAGCTGAAAGGGAATTCAGAGGCTTTTGTGACTGC 534
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 535 CTGGTTAAGATCTACAAATCTGATGGGATTAAGGGCTGTACCAAGGCTTTTATGTGTCA 594
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 595 GTGAGGCGCAATATCATCTACCGTGTGCTTCTGCTATCTGATCTATGACACTGCAAGGGA 654
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 655 ATGCTCCGCGATCCCAAGAAATCTCATCTTTCATCAGCTGGATGATTCACAGTCTGTC 714
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 715 ACTGCTGTGCTGCGCTAACTTCTTATCTCTTTGACACCGGTTGCGCGTGTATGATGATG 774
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 775 CAGTCTGGAGCAAGGAAGTGTATATCATGATACAGGCAAGCTTGTGCTGCGGGAAG 834
QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
Db 835 ATCGCTCGAGCAAGGAGGCAAGGCTTTTTCAGGGTGCATGTTCCAAACGTTCTCAGA 894
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
Db 895 GGCATGGTGGTGGCTTTTGCTTGTGATGATGAATCAAGAAAG 942

RESULT 13

US-10-403-571-153
; Sequence 153, Application US/10403571
; Publication No. US20040068763A1
; GENERAL INFORMATION:
; APPLICANT: HOPKINS, Nancy
; APPLICANT: GOLLING, Gregory
; APPLICANT: Amsterdam, Adam
; APPLICANT: Sun, Zhaoxia
; TITLE OF INVENTION: Developmental Mutations in Zebrafish
; FILE REFERENCE: 01997/539002
; CURRENT APPLICATION NUMBER: US/10/403,571
; CURRENT FILING DATE: 2003-03-25

```
; PRIOR APPLICATION NUMBER: US 60/368,760
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 1243
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-403-571-153

Alignment Scores:
Pred. No.: 6,79e-189 Length: 1243
Score: 1446.00 Matches: 274
Percent Similarity: 96.98% Conservative: 15
Best Local Similarity: 91.95% Mismatches: 3
Query Match: 93.71% Indels: 0
DB: 13 Gaps: 0

US-09-811-094-33 (1-298) x US-10-403-571-153 (1-1243)
Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAala 20
Db 45 ATGAGTGAGACCGCATCTCTTCGCCAAGGACATCTTGGCCGGTGATTCGCCGCTGCC 104
Qy 21 IleSerLysThrAlaValAlaProIleGluArgVallLysLeuLeuGlnValGlnHis 40
Db 105 ATCTCAAACCGCGTGGCCCCATTTGAGAGAGTCAAACTGCTGCTTCAGGTGCAACAT 164
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 165 GCTAGCAACACAGATTACAGCAGATAGCAGTACAGGCGCATATGAGTCTGCGTGGTGGT 224
Qy 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 225 ATCCCAAGGAGCGGGCTTCTGCTGCTTCTGGAGAGAACTTGGCCAACTGATCAGATCAGA 284
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 285 TACTTCCCCACACAGCGCTCAACTTTGCTTTTCAAGGACAGTACAAAGAGGCTTCCCTT 344
Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 345 GATGTGTGGACAGCGCCAGCTTTTGGAGGTACTTGGTGTGTAACCTGGCTTCAGGT 404
Qy 121 GlyAlaAlaGlyAlaThrSerLysCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 405 GGTGTGCTGTGTCACATCCCTCTGCTGCTGATCCCTTGACTTCGCAAGAACCCGT 464
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 465 CTGTGTCGGATGTCGGAAGAGTGGACGACAGAGAGAGTTCAGTGGCGCTGGGTAACATGC 524
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 525 TTGTAAGAATCTCCAATCTGATGGCATCAAGGCTGTGACCGAGGCTTCAACGTGTC 584
Qy 181 ValGlnGlyIleIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 585 GTGAGGGTATCATCATTTACAGAGCTGCCTTACCTTCGGCATTTATGACACAGCAAGGGT 644
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 645 ATGTGCCCCGATCCCAAGACACCCATATGTTGTGAGTTGGATGATGCTTCAGAGTGTG 704
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 705 ACTGCTGTGTGCTCTTCTCTACCTACCTTCGACACAGTGGCTCGTCTGATGATGATG 764
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 765 CAGTCTGACGTAAGAGGCTGACATCATGTACAGTGGCAATATGACTCTCTCGAGGAAG 824
Qy 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
; PRIOR APPLICATION NUMBER: US 09/917,800A
; Sequence 1327, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; -APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Blashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1327
; LENGTH: 1196
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 D12770
US-09-917-800A-1327

Alignment Scores:
Pred. No.: 6,97e-186 Length: 1196
Score: 1424.00 Matches: 267
Percent Similarity: 95.64% Conservative: 18
Best Local Similarity: 89.60% Mismatches: 13
Query Match: 92.29% Indels: 0
DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x US-09-917-800A-1327 (1-1196)
Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAala 20
Db 76 ATGGGGATCAGGCTTTCAGGCTTCCTTAAGGACTTCTCGGACGCTGCGATCGCCGCC 135
Qy 21 IleSerLysThrAlaValAlaProIleGluArgVallLysLeuLeuGlnValGlnHis 40
Db 136 GTCTCAAAGACCGCGTCCGCCGATCGAGAGGCTCAAACTGCTGCTGCAGGTCCAGCAT 195
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 196 GCCACAAACAGATCATGTGACAGAAACAGTACAAAGCATCATGATTGTGCTGTGAGA 255
Qy 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
; 825 ATCGCACGTGATGAGGCTGGCAAGGCTTCTTCAAGGGAGCGCTGCTCAACGTTCTCAGA 884
; 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
; 885 GGCATGGGTGGCGCTTTGTGCTGCTGTGATGATGAGCTGAAGAAGGTCAATT 938

RESULT 14
US-09-917-800A-1327
; Sequence 1327, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; -APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Blashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1327
; LENGTH: 1196
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 D12770
US-09-917-800A-1327

Alignment Scores:
Pred. No.: 6,97e-186 Length: 1196
Score: 1424.00 Matches: 267
Percent Similarity: 95.64% Conservative: 18
Best Local Similarity: 89.60% Mismatches: 13
Query Match: 92.29% Indels: 0
DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x US-09-917-800A-1327 (1-1196)
Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAala 20
Db 76 ATGGGGATCAGGCTTTCAGGCTTCCTTAAGGACTTCTCGGACGCTGCGATCGCCGCC 135
Qy 21 IleSerLysThrAlaValAlaProIleGluArgVallLysLeuLeuGlnValGlnHis 40
Db 136 GTCTCAAAGACCGCGTCCGCCGATCGAGAGGCTCAAACTGCTGCTGCAGGTCCAGCAT 195
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 196 GCCACAAACAGATCATGTGACAGAAACAGTACAAAGCATCATGATTGTGCTGTGAGA 255
Qy 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
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Db 256 ATCCCAAGGACAGGGCTTCTCTCCCTTCTGGAGGGTAACCTGGCCAAAGTGTATCCGG 315
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 316 TACTTCCCAACCCAGCTCTCAACTTCGCTTCAAGGACAAGTACAAGCAGATCTTCTGT 375
Qy 101 GlyGlyValAspLysHisThrClnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 376 GGAGGTGTGATCGCAAGAGTCTGGCGCTACTTCGCTGGTAACCTGGCTCTGGT 435
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 436 GGGGAGCTGGGGCTACCTCCTCTGCTTCTGCTACCCACTGGACTTTGCTAGACCCAGG 495
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGlnArgGluPheArgGlyLeuGlyAspCys 160
Db 496 CTGGGTGGCAGCTGGGCAAGGATCTTCCCAAGCGTGTAGTTCAATGGGCTGGGTGACTGT 555
Qy 161 LeuValLysIleThrLysSerAspGlyLysArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 556 CTCACCAAGATCTTCAAGCTGTATGGCTGAGGGTCTCTACCGAGGTTCAGTGTCTCT 615
Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 616 GTGAGGGCATCATCATCTACAGAGCTGCTACTTCGGAGTCTATGACACTGCCAAGGG 675
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 676 ATGCTGCCAGACCCCAAGATGTGCACATTAATGTGAGCTGATGTCCACAGGTGTG 735
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 736 ACAGCCGTGGGGGCTGGTGTCTCATTTTGACACTGTCCGTGTAGATGATGATG 795
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 796 CAGTCTGGCCGAAGGGCTGATATTATGTATGATGATGATGATGATGATGATGATG 855
Qy 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyValAlaTrpSerAsnValLeuArg 280
Db 856 ATTCGAAGATGAGGACGCAAGCTTCTTCANAGGTGTCTGTCACAGCTACTGGA 915
Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValle 298
Db 916 GCATGGGGGTGCTTTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGTATTGT 969
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RESULT 15

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US-10-198-846-13437
; Sequence 13437, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13437
; LENGTH: 1711
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405,
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; LOCATION: 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415,
; LOCATION: 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425,
; LOCATION: 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1435-1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444,
; LOCATION: 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13437
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Alignment Scores:

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Pred. No.: 1,43e-183 Length: 1711
Score: 1409.00 Matches: 263
Percent Similarity: 94.63% Conservative: 19
Best Local Similarity: 88.26% Mismatches: 16
Query Match: 91.32% Indels: 0
DB: 15 Gaps: 0
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US-09-811-094-33 (1-298) x US-10-198-846-13437 (1-1711)

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Qy 1 MetThrGluClnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaA 20
Db 167 ATGGGTGATCACCGCTTGGAGCTTCTTAAAGGACTTCTGGCCGGGGCGCTCGCGTGC 226
Qy 21 IleSerLysThrAlaValAlaPheGluArgValLysLeuLeuLeuGlnValGlnHis 40
Db 227 GTCTCCAAGACCGGGTGGCCCCCATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT 286
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 287 GCCAGCAACAGATCATGTCTGAGAGGAGTACAAAGGGATCATATTGTTGTGTGTGAGA 346
Qy 61 IleProLysGlnGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 347 ATCCCTAAGAGACAGGGCTTCTCTCTCTGAGGGGTAACTGCCCAACGATGATCCGT 406
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 407 TACTTCCCCACCAAGCTCTCAACTTCGCTTCAAGGACAAAGTACAAAGCAGCTCTTCTTA 466
Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 467 GGGGGTGTGATCGCATAGCAGTCTTGGCGCTACTTTGCTGTGAACCTGGCGTCCGGT 526
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 527 GGGGCGCTGGGGCCACTTCTTGTCTTGTCTACCGCTGACCTTGTAGACACAGG 586
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 587 TTGGCTGCTGATGGGCAAGGGCGGCGGCGGCGGCTTACCGAGGTTCACAGCTCTCT 646
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 647 ATCATCAAGATCTTCAAGTCTGATGGCTGAGGGGGCTTACCGAGGTTCACAGCTCTCT 706
Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 707 GTCCAGGCATCATATCATATAGAGTCTTCTTCTGAGTCTATGATATGATGATGATGATG 766
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 767 ATGCTGCTGACCCCAAGAACGTGCACATTTTGTGAGCTGGATGATTTGCCCAAGATG 826
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 827 ACGGCAGTGGCAGGGTGGTGTCTTACCCCTTTTGACACTGTTCTGCTGATGATGATG 886
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 887 CAGTCCCGCGGAAGGGCGGATATTATGTATACCGGGGACAGTGTGCTGCTGAGGAAG 946
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QY      261  IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValIleuArg 280
Db      947  ATTGCAAAAGACGAAGGAGCCAGGCGCTTCTTCAAGGTGGCTGGTCCAAIGTGTCTGAGA 1006

QY      281  GlyMetGlyGlyAlaPheValIleuValLeuTyrAspGluLeuLysLysValIle 298
Db      1007  GGCATGGCGGTGCTTTTGTATTGGTGTGTATGATGAGATCAAAAAAATATGTC 1060
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Search completed: August 17, 2004, 21:40:56
Job time : 543 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2004, 17:56:49 ; Search time 2930 Seconds
(without alignments)
3037.177 Million cell updates/sec

Title: US-09-811-094-33
Perfect score: 1543
Sequence: 1 MTEQAISPAKDFLAGGIAAA.....LRMGGAFLVLYDELKKVI 298

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO spool/US09811094/runat 10082004_105413_12472/app_query.fasta_1.455
-DB=EST -OPMT=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bics -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09811094 @CGN_1_13437 @runat 10082004_105413_12472 -NCFU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_man.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_pbg.*
27: em_gss_vrl.*
28: gb_gssi.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1543	100.0	1355	11	BC013256	BC013256 Homo sapi
2	1543	100.0	1355	11	BC035469	BC035469 Homo sapi
3	1474	95.5	1201	13	EX419742	EX419742 BX419742
4	1463	94.8	1201	13	EX353661	EX353661 BX353661
5	1458	94.5	1201	9	AL545701	AL545701 AL545701
6	1454.5	94.3	1201	9	AL534908	AL534908 AL534908
7	1452.5	94.1	1071	12	BM554606	BM554606 AGENCOURT
8	1451	94.0	949	13	BQ932832	BQ932832 AGENCOURT
9	1451	94.0	1218	14	CF110898	CF110898 Shultzomi
10	1449	93.9	1201	9	AL540267	AL540267 AL540267
11	1445	93.6	1237	11	AK012951	AK012951 Mus muscu
12	1445	93.6	1237	11	AK088730	AK088730 Mus muscu
13	1445	93.6	1239	11	AK003467	AK003467 Mus muscu
14	1440	93.3	1015	13	BX360934	BX360934 BX360934
15	1438	93.2	1064	14	CK024940	CK024940 AGENCOURT
16	1436	93.1	1185	9	AL515693	AL515693 AL515693
17	1435	93.0	1130	14	CF660610	CF660610 CCLX07a30
18	1434	92.9	1201	13	BX424943	BX424943 BX424943
19	1432	92.8	1145	14	CK025379	CK025379 AGENCOURT
20	1432	92.8	1201	13	BX395578	BX395578 BX395578
21	1431	92.7	1045	13	BX420955	BX420955 BX420955
22	1428	92.5	1160	14	CK025422	CK025422 AGENCOURT
23	1426	92.4	1171	14	CF111068	CF111068 Shultzomi
24	1421	92.1	911	13	EX708727	EX708727 BX708727
25	1418	91.9	1201	9	AL557414	AL557414 AL557414
26	1418	91.9	1201	13	BX462646	BX462646 BX462646
27	1417	91.8	1106	14	CK025329	CK025329 AGENCOURT
28	1416	91.8	1201	9	AL539376	AL539376 AL539376
29	1414	91.6	1295	11	AK078077	AK078077 Mus muscu
30	1410	91.4	959	13	BX705948	BX705948 BX705948
31	1410	91.4	1006	13	EX704347	EX704347 BX704347
32	1410	91.1	1014	13	BX375536	BX375536 BX375536
33	1404	91.0	937	13	BX706933	BX706933 BX706933
34	1404	91.0	1090	13	BX457520	BX457520 BX457520
35	1400	90.7	931	13	BQ933670	BQ933670 AGENCOURT
36	1400	90.7	1201	9	AL514420	AL514420 AL514420
37	1398	90.6	1119	13	BUS15488	BUS15488 AGENCOURT
38	1396	90.5	1209	14	CD496256	CD496256 CDA21-C08
39	1394	90.3	956	13	EX703901	EX703901 BX703901
40	1393	90.3	1201	13	BX464683	BX464683 BX464683
41	1392	90.2	1236	11	AK002283	AK002283 Mus muscu
42	1390	90.1	921	13	BX708871	BX708871 BX708871
43	1389	90.1	999	13	BX411074	BX411074 BX411074
44	1389	90.0	1146	14	CD509246	CD509246 CDA95-C07
45	1388	90.0	931	13	BX728888	BX728888 BX728888

ALIGNMENTS

RESULT 1

BC013256

LOCUS

DEFINITION

BC013256 1355 bp mRNA linear HTC 17-DEC-2003
Homo sapiens solute carrier family 25 (mitochondrial carrier;
adenine nucleotide translocator), member 6, mRNA (cDNA clone
IMAGE:3865895).

ACCESSION

BC013256

VERSION

BC013256.1

KEYWORDS

HTC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 1355)
 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
 Altshul,S.F., Zesberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
 Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
 Stapleton,M., Soares,M.B., Bonaldo,M.P., Cabavant,T.L.,
 Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
 Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
 Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
 Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
 Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
 Fahy,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S.,
 Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932

2 (bases 1 to 1355)
 Strausberg,R.

REFERENCE
AUTHORS
TITLE
JOURNAL

Direct Submission
 Submitted (27-AUG-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-remail.nih.gov
 Tissue procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 13 Row: e Column: 10
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4507746
 This clone has the following problem: no 5' EST match.

FEATURES

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3865895"
 /tissue_type="Eye, retinoblastoma"
 /clone_lib="NIH MGC 67"
 /lab_host="DH10B"
 /note="vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:
 Pred. No.: 1.43e-179 Length: 1355
 Score: 1543.00 Matches: 298
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-811-094-33 (1-298) x BC013256 (1-1355)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
 Db 92 ATGACGGAAACAGGCCATCTCTTCGCGCAAGACTTCTTGGCGGAGGCATCGCGCGCGC 151
 QY 21 ILeSerIysThrAlaValAlaProIleGluArgValLysLeuLeuGlnHis 40
 Db 152 ATCTCAAGACGCGCGTGGTCCGATCGAGCGGGTCAAGCTGCTGCTGAGGTCCAGCAC 211
 QY 41 AlaSerLysGlnIleAlaAlaLysGlnIleLysGlyIleValAspCysIleValArg 60
 Db 212 GCCAGCAAGCAGATCGCGCCGACAGCAGTCAAGGGCATCGTGACATGATTCGCGC 271
 QY 61 ILeProIysGluGlnIleValLeuSerPheThrArgGlyAsnLeuAlaValIleArg 80
 Db 272 ATCCCCAAGAGCAGGGCGTGTCTCTTCGAGGGGCAACCTTGCACACGTCATTCGC 331
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
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 QY 101 GlyGlyValAspLysHisThrGlnPheThrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
 Db 392 GGGGGCGTGGACAAAGCACACGAGTTCTCGAGGTACTTTTCGGGGCAACCTGGCCCTCGGC 451
 QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaThrArg 140
 Db 452 GTGCGCGCGCGCGACCTCCCTCTGCTGTGTACCGCTCGATTTTCGCCAAGACCCGCG 511
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 Db 512 CTGGCAGCGGACGTTGGGAAAGTCAGGCACAGACGCGAGTTCGAGGCGCTGGAGACTGC 571
 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 Db 572 CTGGTGAAGATCACCAGTCCCGACGCGCATCCGGGCGCTGTACCGAGGCTTTCAGTGTCTCC 631
 QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
 Db 632 GTGAGGGCATCATCATCTACCGGGCGGCTACTTTCGGCGTGTACGATACGGCCAGGGC 691
 QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
 Db 692 ATGCTCCCGACGCCAAGAACACGACATCATGACACGGCCACCGTGCATGTCGAGCAGCGTG 751
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 Db 752 AGCGCGTGGCGCGGTGGTGTCTTACCCCTTCGACAGGTCGCGCGCGCATGATGATG 811
 QY 241 GlnSerGlyArgGlyGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
 Db 812 CAGTCCGGCGCGCAAGAGGAGTCATCATGATACACGGCCACCGTGCATGTTGGAGGAAG 871
 QY 261 ILePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
 Db 872 ATCTTCAGATGAGGGGGGCAAGGCTTCTTCAGGGTGGTGTGTCACAGCTCTCTCGCG 931
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
 Db 932 GGCATGGGGGGCGCTTCGTGCTGCTGCTGTACGACGAGCTCAAGAGGTGATC 985

RESULT 2

BC035469
 LOCUS
 DEFINITION
 Homo sapiens solute carrier family 25 (mitochondrial carrier;
 adenine nucleotide translocator), member 6, mRNA (cDNA clone
 IMAGE:3867130).
 ACCESSION
 BC035469
 VERSION
 BC035469.1
 KEYWORDS
 GI:22028373
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1355)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stalteron,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahy,J., Helton,E., Kertanen,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickinson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Kryzyski,M.I., Skalska,U., Smallus,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBLISHED 12477932

REFERENCE 2 (bases 1 to 1355)
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 1A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabbs-r@mail.nih.gov
 Tissue procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: ang@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
 Series: IRAX Plate: 13 Row: f Column: 9
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4503556
 This clone has the following problem: no 5' EST match.

FEATURES
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 /db_xref="taxon:9606"
 /clone="IMAGS:3867130"
 /tissue_type="Eye, retinoblastoma"
 /clone_lib="NIH MGC_67"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORTs"

ORIGIN
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 Score: 1543.00 Matches: 298
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-811-094-33 (1-298) x BC035469 (1-1355)

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 Db 92 ATGACGGAAAGAGGCACTCTCTTCGCCAAAGACTTCTTGGCCGAGGACATCGCGCGGCC 151
 QY 21 IleserLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
 Db 152 ATCTCCAAGACGGCGCTGGCTCGATCGAGCGGTCAAGCTGCTGCTGCTGAGGTCCAGCAC 211
 QY 41 AlaserLysGlnIleAlaAlaAspLysGlnTyrlsGlyIleValAspCysIleValArg 60
 Db 212 GCCAGCAGCAGATCGCGCGGCAAGCAGTACAAGGGCATCGTGGACTCATGTGTCGCG 271
 QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
 Db 272 ATCCCCAAGGAGCGGCGTCTGCTCTTGGAGGGGCAACCTTGCACAGTCATTCGC 331
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrlsGlnIlePheLeu 100
 Db 332 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAAGTACAAGCAGATCTTCCTG 391
 QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrlsPheAlaGlyAsnLeuAlaSerGly 120
 Db 392 GGGGCGGTGGACAAGCAGCAGCTTCTGGAGGTACTTTGGGGGCAACCTTGGGCTCGGC 451
 QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrlsProLeuAspPheAlaArgThrArg 140
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 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
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 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrlsGlnGlyPheSerValSer 180
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 QY 181 ValGlnGlyIleIleIleTyrlsArgAlaAlaTyrlsPheGlyValTyrlsAspThrAlaLysGly 200
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 QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
 Db 692 ATGTCTCCGACCCCAAGAACACACCATCGTGTGTAGCTGGATGATCGGCACACCGTG 751
 QY 221 ThrAlaValAlaGlyValValSerTyrlsPheAspThrValArgArgArgMetMetMet 240
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 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrlsThrGlyThrValAspCysTrpArgLys 260
 Db 812 CAGTCCGCGCGCAAGGAGCTGACATCATGTACAGGCGACCGTCTGACTGTGTGAGGAAG 871
 QY 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
 Db 872 ATCTTCAGAGATGAGGGGGCAAGGCTTCTTCAAGGGTGTGCTGTCCAAGCTCTCGCG 931
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrlsAspGluLeuLysValIle 298
 Db 932 GGCATGCGGGCGCGCTTCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 985

RESULT 3
 LOCUS BX419742 1201 bp mRNA linear EST 13-MAY-2003
 DEFINITION BX419742 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 CS0DF020YC16 5-PRIME, mRNA sequence.
 ACCESSION BX419742
 VERSION BX419742.1 GI:30642547
 EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1201)

161	LeuValIyleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer	180
632	CTGGTGAAGATACCAAGTCCGACGGCATCCGGGGCTGTACAGGGCTTCAGTGTCTCC	691
181	ValGlnGlyIleIle-IleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysG1	200
692	GTGACGGGATCATATCATCTACCGGGCGGCTACTTCGGCGGTGTACGATACGCGCAAGG	751
200	YMetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVa	220
752	CATGCTCCCGACCCCAAGAACACGACATCGTGGTGGTGGATGATCGCGACACCGT	811
220	lThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMe	240
812	GACGGCGGTGGCGGGTGGTGTCTTACCCCTTCGACACGGTGGCGCGCATGATGAT	871
240	tGlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgly	260
872	GCACTCCGGGCGCAAGAGAGCTGCATCATGACCGGGCAGCTCGGACTGTGGAGGAA	931
260	silePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuAr	280
932	GATCTTCAGATGACGGGGGCAAGGCTTCTTCAAGGTGGTGGTCCAAAGCTCTCGG	991
280	gGlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValle	298
992	GGGCATGGGGGGGGCTTCGTGCTGTGTGTACGACGAGCTCAARAGGTGATC	1046
Qy	RESULT 4	
Db	BX353661	
Qy	DEFINITION	
Db	BX353661 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens	
Qy	LOCUS	1201 bp mRNA linear EST 05-MAY-2003
Db	CDNA clone CS0DC010YK03 5-PRIME, mRNA sequence.	
Qy	ACCESSION	BX353661
Db	VERSION	BX353661.1 GI:30375795
Qy	KEYWORDS	EST.
Db	SOURCE	Homo sapiens (human)
Qy	ORGANISM	Homo sapiens
Db	REFERENCE	1 (bases 1 to 1201)
Qy	AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Db	TITLE	Full-length cDNA libraries and normalization
Qy	JOURNAL	Unpublished (2001)
Db	COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 11066.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DC010AF02QPl&cluster=11066.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DC010AF02QPl.
Qy	FEATURES	
Db	source	1..1201 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DC010YK03" /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
Qy	ORIGIN	
Db	Alignment Scores:	
Qy	Pred. No.:	9.46e-170 Length: 1201
Db	Score:	1463.00 Matches: 275
Qy	Percent Similarity:	97.66% Conservative: 0
Db	Best Local Similarity:	97.66% Mismatches: 6
Qy	Query Match:	95.53% Indels: 2
Db	DB:	13 Gaps: 0
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Qy	1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAla	20
Db	153 ATGACGGAACAGCGCATCTCTTCGCGCAARATTTCTTGGCGGAGS-ATCGCGCGCGCM	211
Qy	21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis	40
Db	212 ATCTCCNAGACGGCGTGGCTCCGATCAGCGGGTCAAGCTGCTGCAGGTTCAGGCAC	271
Qy	41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg	60
Db	272 GCCAGCAACAGATCGCCCGCCACAGCAGTACAGAGGCATCGTGGACTGATGTCGCG	331
Qy	61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg	80
Db	332 ATCCCCAGACGACGGCGTGTGCTCTCTGAGGGGCAACCTTGCMAACGTTCATTCGC	391
Qy	81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu	100
Db	392 TACTTCCCCACTCAAGCCCTCAACTTCGCCCTTCAAGGATAAGTCAAGCAGATCTTCCTG	451
Qy	101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly	120
Db	452 GGGGGCGTGGACACACGAGTCTTGGAGGTACTTTTGGGGCAACCTGGCTCCGCGC	511
Qy	121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg	140
Db	512 GGTGGCGGGCGCGGAMCTCCCTCTGCTGTGTACCGCGCTGGATTTGCCAGAACCCGC	571
Qy	141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys	160
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Qy	Alignment Scores:	
Db	Pred. No.:	9.46e-170 Length: 1201
Qy	Score:	1463.00 Matches: 275

Percent Similarity:	97.30%	Conservative:	13
Best Local Similarity:	92.91%	Mismatches:	8
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QY	21	IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis	40
DB	188	ATCTCAAGACCGCGGTAGCGCCATCGAGCGGGTCAAGCTCTCTGCGAGTGCAGCAT	247
QY	41	AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg	60
DB	248	GCCAGACAGACATCACTGCAGATAGCAATCAAGGCAATATAGACTGGTGGTCCGT	307
QY	61	IleProLysGluGlnGlyValLeuSerPheThrArgLysAsnLeuAlaAsnValIleArg	80
DB	308	ATTCCCAAGAGCAGGAGGTCTGTCTTCTGCGCGGTAACTGGCCAAATGTCATCAGA	367
QY	81	TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu	100
DB	368	TACTTCCCAACCGAGCTCTTAACCTTCGCTTCAAGATTAATACAGCAGATCTTCCTG	427
QY	101	GlyGlyValAspLysHisThrGlnPheThrArgTyrPheAlaGlyAsnLeuAlaSerGly	120
DB	428	GCTGGTGTGGACAAAGAACCCAGATTTCGCGCTACTTTGCAGGGAATCTGGCATCGGT	487
QY	121	GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaThrArg	140
DB	488	GCTGCGCGAGGCGCCACATCCCTGTGTTGTGTACCTCTTGATTTGCGCGTACCCGT	547
QY	141	LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys	160
DB	548	CTAGCAGCTGATGTGGTAAACTGGAGCTGAAGGGAATTCGAGGCTCGTCACTGC	607
QY	161	LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer	180
DB	608	CTGGTTAAGATCTACAAATCTGATGGGATTAAGGCGCTGTACCAAGGCTTTAACTGTCT	667
QY	181	ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly	200
DB	668	GTCAGGGTATTATCATCTACCGAGCGGCTACTTCGGTATCTATGACACTGCAAGGA	727
QY	201	MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal	220
DB	728	ATGCTTCGGATCCCAAGAACACTCACATCGTCATCAGCTGGATGATCGACAGACTGTC	787
QY	221	ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetKet	240
DB	788	ACTGCTGTGCGCGGGTGTACTTCCTATCCATTGTACACCGTTCGCGCGCATGATGATG	847
QY	241	GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys	260
DB	848	CAGTCAGGCGCAAGGAAGTACATCATGTACACAGGCACGCTTGACTGCTGGCGAAG	907
QY	261	IlePheArgAspGlnGlyLysAlaPhePheLysGlyAlaTrpSerAsnValIleArg	280
DB	908	ATTGCTCGTATGAAGAGGCAAGCTTTTTCATAGGGTGCATGTGTCATGTTCTCAGA	967
QY	281	GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys	296
DB	968	GGCATGGTGGTCTTTTGCTGTCTTGTATGATGAATCAAGAA	1015
RESULT 5	AL545701		
LOCUS	1201 bp mRNA linear EST 31-MAY-2003		
DEFINITION	AL545701 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA		
ACCESSION	AL545701		

VERSION	AL545701.2	GI:31267536
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	Unpublished (2001)	
COMMENT	On Feb 15, 2001 this sequence version replaced gi:12878183. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqraf@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10389.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DI009CD02QP1&cluster=10389.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue Genoscope sequence ID : CS0DI009CD02QP1.	
FEATURES	Location/Qualifiers	
Source	1..1201	
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	/notes="First strand cDNA was primed with a NotI-oligo (GT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	
ORIGIN		
Alignment Scores:		
Pred. No.:	3,93e-169	Length: 1201
Score:	1458.00	Matches: 290
Percent Similarity:	97.32%	Conservative: 1
Best Local Similarity:	96.99%	Mismatches: 6
Query Match:	94.49%	Indels: 3
DB:	9	Gaps: 0
US-09-811-094-33 (1-298) x AL545701 (1-1201)		
QY	2	ThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaIle 21
DB	51	TCCCGGGATGCATCTCTTCCGCAAGACTTCTTGGCGGACGCTNCGCGCGCCATC 110
QY	22	SerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHisAla 41
DB	111	TCCAAGACGGCGGTGCTCGATCGAGCGGGTCAAGCTGTCTGTCAGGTCACGACGCC 170
QY	42	SerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArgIle 61
DB	171	AGCAAGCAGATCGCGCGCGCAGCAGCAGTACAAAGGCACTCGTGGACTCAITTCGCA 230
QY	62	ProLysGlnGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArgTyr 81
DB	231	CCCAGGAGCAGCGGCTGCTCTTGGAGGGGCACTTGGCAACGCAITTCGCTAC 290
QY	82	PheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeuGly 101
DB	291	TTCCCCACTCAAGCCCTCACTTCGCTTCAAGGATTAAGTACAGCAGATCTTCTCGGG 350
QY	102	GlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGlyGly 121
DB	351	GCGCTGGCAAGCAGCAGCTTCTGAGGTACTTTTCGGGCAACCTGGGCTCGCGGGT 410
QY	122	AlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArgLeu 141

Db 411 GCGGCGCGCGGACCTCCTCTGCTTGTGTACCGCTGGATTTCCGACAGAACCCGCTG 470

QY 142 AlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCysLeu 161

Db 471 GCAGCGAGCTGGAAAGTCAGGCACAGAGCGGAGTTCGAGAGCTGGAGACTGCCTG 530

QY 162 ValValIleThrLysSerAspGlyIleArgGlyLeuTyrglnGlyPheSerValSerVal 181

Db 531 GTGAAGATCACCAAGTCCGACGGCATCCGGGCGCTGTACACAGGCTTCAGTGTCTCCGTG 590

QY 182 GlnGlyIleIleLeuTyrglnAlaAlaValPheGlyValTyrglnAlaLysGlyMet 201

Db 591 CAGGGCATCATCTACCGGCGGCGCTACTTCGGCGGTGTACGATACGGCCPAGGGCATG 650

QY 202 LeuProAspProLysAsnThrHisLeuValSerTrpMetIleAlaGlnThrValThr 221

Db 651 CTCGCCGACCCCAAGAACACGACATCGTGTGTAGCTGTGATGTCGCGACACCGTGCAG 710

QY 222 AlaValAlaGlyValValSerTyrglnPheAspThrValArgArgMetMetMetGln 241

Db 711 GCGGTGGCGGCGGTGTCTTACCTTCGACAGGTGGCGCGCGCATGATGATGCAG 770

QY 242 SerGlyArgGlyGlyAlaAspIleMetTyrglnThrValAspCysTrpArgLysIle 261

Db 771 TCCGGCGGCAAGAGAGCTGACATCATGTACACGGCGCAGTTC - GACTGTTGGAGGAGATC 829

QY 262 PheArgAspGluGlyGlyValAlaPhePheLysGlyAlaTrpSerAsnValLeuArgGly 281

Db 830 TTCAGAGATGAGGGGGGAGCGCTTCTCAAGGCTGTGTCTCAAGCTCTCGGGGG 889

QY 282 --MetGlyGlyAlaPheValLeuValLeuTyrglnAspGluLeuLysLysValIle 298

Db 890 CATGGCGGGGGCGCTCTGCTGTGCTGTACGACGAGCTCAAGAAGTGTATC 942

RESULT 6

AL534908 1201 bp mRNA linear EST 12-MAY-2003

LOCUS AL534908 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone

DEFINITION CS0DF007Y120 5-PRIME, mRNA sequence.

ACCESSION AL534908

VERSION AL534908.2 GI:30541165

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li W.B., Gruber, C., Jessee, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 13, 2001 this sequence version replaced gi:12798401.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10389.r For more information about this cluster, see

http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF007BE10P1&cluster=10389.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DF007BE10Q1.

Location/Qualifiers

1..1201

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/mol_type="mRNA"

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/clone="CS0DF007Y120"

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/clone_lib="Homo sapiens FETAL BRAIN"

/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA"

FEATURES

source

was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.: 1,07e-168 Length: 1201

Score: 1454.50 Matches: 293

Percent Similarity: 97.99% Conservative: 0

Best Local Similarity: 97.99% Mismatches: 5

Query Match: 94.26% Indels: 3

DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x AL534908 (1-1201)

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Db 161 ATGACGGAACAGGCCATCTCTTCGCAAGAGCTTCTTGCGCGAS--ATCGCGCGCGCC 218

QY 21 IleSerLysThrAlaValAlaPheGluArgValLysLeuLeuGlnHis 40

Db 219 ATCTCCAAGACGCGCGTGTCTCCGATCGASCAGGTCAGCTGCTGTCGAGGTCCAGCAC 278

QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrglnValValAspCysIleValArg 60

Db 279 GCCAGCAGCAGATCCGCCCGCACAGCAGTACAGGGCATCTGTGAGCTGCATTGTCCGC 338

QY 61 IleProLysGlnGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80

Db 339 ATCCCAAGAGCAGCGCGTGTCTCTTCGAGGGGCAACCTTGCCACCTCATTCGC 398

QY 81 TyrglnProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrglnIlePheLeu 100

Db 399 TACTTCCCTCCTCAAGCCCTCAACTTCGCTTCAAGGATPAAGTACAGCAGATCTTCTTG 458

QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrglnPheAlaGlyAsnLeuAlaSerGly 120

Db 459 GGGGGCGTGGACAAAGCACACGACAGTTCGAGGTACTTTTGGGGGCAACCTTGCCCTCCGC 518

QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrglnPheAlaAspPheAlaArgThrArg 140

Db 519 GGTGCGCGCGCGCGACCTCTCTGCTTGTGTACCGCTCGATTTCGCCAGAACCCGCG 578

QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160

Db 579 CTGGCAGCGGAGCTGGAAAGTCAGGCACAGACGCGAGTTCGAGGCTTCGGAGACTGC 638

QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrglnGlnGlyPheSerValSer 180

Db 639 CTGCTGAAGATCACCAAGTCCGACGCGCATCCGGGCGCTGTACCGAGGCTTCAGTGTCTCC 698

QY 181 ValGlnGlyIleIleLeuTyrglnAlaAlaTyrglnValTyrglnAspThrAlaLysGly 200

Db 699 GTGCAGGGATCATCATCTACCGCGCGCGCTTCTTCCGGCTGTACATACGCGCGAGGCG 758

QY 201 MetLeuProAspProLysAsnThrHisLeuValSerTrpMetIleAlaGlnThrVal 220

Db 759 ATGTCTCCCGACCCCAAGAACACGACATCATCTGTGTGTGAGCTGATGTCGCGCAGACCGTG 818

QY 221 ThrAlaValAlaGlyValValSerTyrglnPheAspThrValArgArgMetMetMet 240

Db 819 AGCGCGGTGGCGCGTGGTGTCTTATCCCTTCGACAGCGGTGGCGCGCATGATGATG 878

QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrglnThrValAspCysTrpArgLys 260

Db 879 CAGTCCGCGCGCAAGAGGAGCTGACATCATGTACACGGCGACGTC - GACTGTTGGAGGAG 937

QY 261 IlePheArgAspGluGlyGlyAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280

Db 938 ATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAAGGGTGTGTGTCTCAAGCTCTCTCGCG 997

QY 281 GlyMet-GlyGlyAlaPheValLeuValLeuTyrglnAspGluLeuLysLysValIle 298

```

Db      998 GGCATGGGGGGCGCTTCGTCGTCCTGTACGACGAGCTCAGAAGGTGATC 1052
|||||
RESULT 7
LOCUS   BM554606                      1071 bp      mRNA      linear      EST 20-FEB-2002
DEFINITION AGENCOURT_6545407 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5736868
5', mRNA sequence.
ACCESSION BM554606
VERSION   BM554606.1 GI:18794346
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 1071)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12746 row: b column: 05
High quality sequence stop: 646.
Location/Qualifiers
1..1071
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5736868"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="PH108 (phage-resistant)"
/clone_lib="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-Sport6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 1
Score: 158e-168 Length: 1071
/db_xref="taxon:9606" Matches: 292
Percent Similarity: 97.34% Conservative: 1
Best Local Similarity: 97.01% Mismatches: 3
Query Match: 94.13% Indels: 5
DB: 12 Gaps: 1

US-09-811-094-33 (1-298) x BM554606 (1-1071)
QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
Db 13 ATGACGGALACAGCCATCTCTTCGCCAAAGACTTCTTGGCCGAGGATCGCCGCC 72
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 73 ATCTCCACAGCGCCGTCGTCGATCGAGCGGGTCAAGCTCTGCTGAGTCCAGCAC 132
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 133 GCACAGACAGATCCGCCGACAGAGTACAGGGGATCGTGGATGCAATTCGCGC 192
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 193 ATCCCCAAGAGCAGCGCGCTGCTCTCTCTGGAGGGGCAACTTGGCAACGTCATCGC 252
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100

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Db      253 TACTTCCCCTCAAGCCCTCAACTTCGCTTCAGGATAAGTACAGCAGATCTTCCTG 312
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 313 GGGGGCGGTGACACAGCACACGAGTCTTGGAGGTACTTTGGCGGCAACTGGGCTCGGC 372
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 373 GGTGGCGCGCGCGACCTCCCTCTGCTCGTACCCGCTGATTTGCGCAGAACCCGC 432
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 433 CTGGCAGCGGACCTGGGAAAGTCAGGCACAGCGGAGTTCGAGGCCCTGGGAGACTGC 492
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 493 CTGGTGAAGATCACCAAGTCCGACGCGCATCCGGGGCTGTACCAAGGCTTCAGTGTCTCC 552
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 553 GTGCAGGCGCATCATCTACTACCGGGCGGCTTCTTGGCGGTGTACGATCGGCAAGGGC 612
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 613 ATGCTCCCCGACCCCAAGAACACGACATCTGCTGGTGGATGATCGCGAGACCGTG 672
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgArgMetMetMet 240
Db 673 ACGGCCGTGGCGCGGTGTGTCTACTACCCCTTCGACACGCGTGGCGGCGCGCATGATG 732
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260
Db 733 CAGTCCGGCGGCAAGAGAGCTGACATCATGACCGGCGACCTCGACTTGTGGAGGAA 792
QY 260 sIlePheArgAspGlu-GlyGlyLysAlaPhePheLysGlyAlaTrp-SerAsnValLeu 279
Db 793 GATCTTCAGAGATCAGGGGGGGGCAAGGCTTCTTCAAGGGTGGTGGTCCAAGCTCTG 852
QY 280 ArgGlyMetGlyGlyAla---PheVal-LeuValLeuTyrAspLeuLysLys 296
Db 853 CGGGGGCATCGGGGGGGCGCCCTTCGTCGCTGGCCCTGTACGACGAAGCTCAGAAG 907

RESULT 8
LOCUS   BQ932832                      949 bp      mRNA      linear      EST 21-AUG-2002
DEFINITION AGENCOURT_8824122 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6459460
5', mRNA sequence.
ACCESSION BQ932832
VERSION   BQ932832.1 GI:22348215
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 949)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2644 row: j column: 05
High quality sequence stop: 674.
Location/Qualifiers
1..949
/organism="Homo sapiens"

FEATURES
Source

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6459460"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_18"
/notes="organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

```

ORIGIN

Alignment Scores:
 Pred. No.: 2e-168 Length: 949
 Score: 1451.00 Matches: 285
 Percent Similarity: 96.98% Conservatve: 4
 Best Local Similarity: 95.84% Mismatches: 7
 Query Match: 94.04% Indels: 2
 DB: 13 Gaps: 0

US-09-811-094-33 (1-298) x BQ932832 (1-949)

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QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
DB 53 ATGACGGAAACAGGCATCTCTCCCAAGACTTCTTGGCGGAGGATCGCGCGGCC 112
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 113 ATCTCCAGAGCGCGTGGCTCCGATCGAGCGGTCAAGCTGCTGCTGAGTCCAGC 172
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 173 GCCAGCAAGCAGATCGCGCGCAGCAAGCAGTACAGGCGCATCGTGGACTGCTGCCG 232
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
DB 233 ATCCCAAGGAGCAGGCGTGTCTCTTGGAGGGCACTTGGCAAGCTCATTCGC 292
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 293 TACTTCCCACTCAAGCCCTCAACTTCGCCCTCAAGGATAAGTACAAGCAGATCTTCTG 352
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 353 GGGGCGTGGACAGCAACGACGAGTCTGGAGGTACTTTGGGGCAACCTGGCGCTCCGCG 412
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
DB 413 GGTGCGCGCGCGACCTCCCTCTGCTTCTGTGTACCGCTGGATTTCGCCAGAACCGCG 472
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 473 CTGGCAGCGGACGCTGGGAAATCAGGCAACAGCGCGAGTTCGAGGCGCTGGGAGATGC 532
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 533 CTGGTGAGATACCAAGTCGAGCGGCATCGGGGCGCTGTACCAAGGCTTCAGTGCTCC 592
QY 191 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 593 GTGAGGGCATCATCATCTACCGCGCGCCCTACTTCGCGGTGTACGATACGGCCAAAGGC 652
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
DB 653 ATGCTCCCGACCCCAAGAACGACATCTGTGTGAGCTGGATGATCGCGCAGACCGTG 712
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
DB 713 ACGGCGGTGGCGCGGTGTCTTACCTACCCCTCGACACGCTGGCGCGCGCATGATGATG 772

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QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCys-TrpArgLys 260
DB 773 CAGTCCGGCGCAAGAGAGCTGACATCATGTACACGGGCACCGTGCAGCTGTGGAGGAA 832
QY 260 sIlePheArgAspGlyGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuAr 280
DB 833 GATCTTCANAGATGAGGGGGGAGGGCCCTCTTCAAAAGTGGTGGTCCACCTCTCGNG 892
QY 280 GGlyMetGlyGlyAla-PheValLeuValLeuTyrAspGluLeuLysLys 296
DB 893 GGGCATGGGGGGCGCTCTGCTGCTGCTGTACGAGACCTCAGAAGG 942

```

RESULT 9

CF110898

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 1218)

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Shultz MA

Dept. of Molecular Biosciences, School of Veterinary Medicine

University of California, Davis

1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA

Tel: 530 752 0793

Fax: 530 752 4698

Email: maschultz@ucdavis.edu

Average Phred score is 20 or better. All poor quality data (Phred <

20) and vector/linker sequence has been removed.

High quality sequence stop: 1218.

FEATURES

source

1..1218

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="Contig3683"

/sex="male"

/tissue_type="airway or parenchyma"

/dev_stage="adult"

/clone_lib="Rat lung airway and parenchyma cDNA libraries"

/note="Organ: lung; Vector: pGEM-lizf(-); Site 1: Eco RI;

Site 2: Not I; mRNA was isolated from microdissected rat

lung airways and parenchyma tissues."

ORIGIN

Alignment Scores:

Pred. No.: 2,96e-168 Length: 1218

Score: 1451.00 Matches: 272

Percent Similarity: 96.98% Conservatve: 15

Best Local Similarity: 91.89% Mismatches: 9

Query Match: 94.04% Indels: 0

DB: 14 Gaps: 0

US-09-811-094-33 (1-298) x CF110898 (1-1218)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20

DB 59 ATGACAGATCGCGTGTCTTCCCAAGGACTTCTTGGTGTGGTGGAGTGGCGCGGCC 118

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QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 119 ATCTCCAGACGGCGTAGCACCCTCAGCGGGTCAAGCTGCTGCTCAGGTGACGAC 178
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 179 GGCAGCAAGCAATACCGGCAGATAGCAATACAGGGCATCATAGATGGGTGGTGGT 238
QY 61 IleProLysGlnGlyValLeuSerPheTyrArgGlyValAsnLeuAlaAsnValIleArg 80
Db 239 ATCCCAAGCAAGACAGGAGTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 298
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 299 TACTTCCCAAGCAAGGAGTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 358
QY 101 GlyGlyValAspLysHisThrGlnPheTyrArgTyrPheAlaGlyValAsnLeuAlaSerGly 120
Db 359 GGTGGTGTGGACAGAGGACCCAGTTTGGCGGTACTTTGACGGGAACTTGGCATCAGGT 418
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 419 GGTGCTGCTGGGCGCACATCTTGTGCTTGTGTACCTCTTGAATTTGCCGCTACCCGT 478
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 479 CTAGCAGCTGATGTGGCAAGCTGGAGCTGAAGGGAATCAAGGGCTTGGTGACTGC 538
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 539 CTGTTTAAGATCTACAAATCTGATGGATTAGGGCTGTACCAAGGCTTTAATGTGCA 598
QY 181 ValGlnGlyIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 599 GTGCAGGCAATATCATCTACCGTGTGCTACTTTCGGTATCATATGACACTGCAAGGGA 658
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTyrMetIleAlaGlnThrVal 220
Db 659 ATGCTCCCGATCCCAAGAAATCTCATCTTCACTGATGATGATGATGATGATGATG 718
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 719 ACTGCTGTTGTGGCTAACTCTTATCTTTTGCACACGGTTCGGCTGCTGATGATG 778
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrPheLys 260
Db 779 CAGTCTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 838
QY 261 IlePheArgAspGluGlyGlyAlaPhePheLysGlyValAlaTyrSerAsnValLeuArg 280
Db 839 ATGCTCTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 898
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuValLeuValLeuValLeuValLeuVal 296
Db 899 GGCATGGTGGTGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 946
RESULT 10
AL540267 1201 bp mRNA linear EST 31-MAY-2003
LOCUS AL540267 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF032YN01 5-PRIME, mRNA sequence.
ACCESSION AL540267
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE (bases 1 to 1201)
JOURNAL Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
PUBLISHED Full-length cDNA libraries and normalization
COMMENT On Feb 15, 2001 this sequence version replaced gi:12870254.
```

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was not normalized. Library was constructed by Life Technologies, a
division of invitrogen. This sequence belongs to sequence cluster
10389.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF032CG01QP1&cluster=10389.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DF032CG01QP1.

FEATURES
source

1..1201
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF032YN01"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/notes="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 5,12e-168 Length: 1201
Score: 1449.00 Matches: 286
Percent Similarity: 98.96% Conservative: 0
Best Local Similarity: 98.96% Mismatches: 3
Query Match: 93.91% Indels: 2
DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x AL540267 (1-1201)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAlaAala 20
Db 159 ATGACGGAACAGGCGCATCTCTTCGCCAAGACTTCTGGCCGAGGATC-GCCGCCGCC 217
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 218 ATCTCCAAGACGGCGTGGCTCCGATCGACGGGTCAAGCTGCTGCTGAGGTCCAGCAC 277
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 278 GCCAGCAAGCAGATCGCCGCGCACAGCAGTACAGGGCATCGTGGACTGCAATGTCGCG 337
QY 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyValAsnLeuAlaAsnValIleArg 80
Db 338 ATCCCAAGCAAGCAGGCGGTGCTGCTCTTGGAGGGGCAACCTTGCACAGTCATTGCGC 397
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 398 TACTTCCCACTCAAGGCCCTCACTTCGCCCTTCAAGGATAAGTACAAAGCAGATCTTCCGT 457
QY 101 GlyGlyValAspLysHisThrGlnPheTyrArgTyrPheAlaGlyValAsnLeuAlaSerGly 120
Db 458 GGGGCGGTGGCAAGCAGCAGCAGTCTTGGAGGTACTTTCGGGCAACCTTGGCCCTCCGCG 517
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 518 GGTGCGCGCGCGCACCTCCCTCTGCTTGTGTACCGCTGGATTTTCGCGAGAACCGCG 577
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 578 CTGCAGCGGACGTGGGAAAGTACAGGCGGAGTTCGAGGCTCCGAGACTGCG 637
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 638 CTGTTGAGATCAACCAAGTCCGACGGCATCGGGGCGCTGTACCGAGGCTTCAGTGTCTCC 697

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics, Wellcome Trust Centre for Molecular Mechanisms in Disease, Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledged. Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>.
URL: <http://fantom.gsc.riken.go.jp/>.

FEATURES

Source

CDS

polyA signal

polvA site

ORIGIN

Alignment scores:

```

Alignment Scores:
Pred. No.:      1.69e-167      length:      1237
Score:          1445.00        Matches:     271
Percent Similarity: 96.62%    Conservative: 15
Best Local Similarity: 91.55% Mismatches:    10
Query Match:    93.65%        Indels:      0
DB:             11           Gaps:        0

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US-09-811-094-33 (1-298) x AK088730 (1-1237)

QY	1	MetThrGluGlnAlaIleSerPheAlaIysAspPheLeuAlaGlyGlyIleAlaAla	20
DB	78	ATGACAGATCGCGTGTCTCTCGCAAGACTTCTTGGCCGCTGAGATGGCGCAGGC	137
QY	21	IleSerLysThrAlaValAlaProIleuArgValLysLeuLeuValGlnHis	40
DB	138	ATCTCCAAGACAGCGGTAGCACCCATCGAGAGGCTCAGCTGCTGTCAGGTGCAGCAT	197
QY	41	AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg	60
DB	198	GCCAGCAAGCAAAATCACGGCAGATAAGCAATACAAGGGCATCATACACTCGCTGTCTGT	257
QY	61	IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg	80
DB	258	ATCCCAAGGAACAGGGAGTCCTCTCTCTTGTGGCGTGGGAACCTGGCCAAATGTCATCAGA	317
QY	81	TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu	100
DB	318	TACTTCCCAACCCAGGCTCTCACTTTGCCTTCAAGATAAATACAAAGCAGATCTTTCTTG	377
QY	101	GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly	120
DB	378	GCTGGTGTGACAGAGGACCCAGTCTCTGGCGCTACTTTGACGGAACTGGCATCAGGT	437


```

Db      861 ATCGCGCGGATGACAGGAGGAGCGCTTTTTCAGAGGCGGCGATGTCACACGTTCTCAGA 920
Qy      281 GlyMetGlyGlyAlaPheValLeuValLeuValLeuValLeuValLeuValLeuValLeu 296
Db      921 GGCAATGGGTGGCGGCTTTTGTGCTTGTCTGTATGATGATGATGATGATGATGATGATGATGAT 968

RESULT 14
LOCUS   BX360934
DEFINITION BX360934 Homo sapiens P1ACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSOD1077YB17 5-PRIME, mRNA sequence.
ACCESSION BX360934
VERSION   BX360934.1 GI:30368462
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1015)
AUTHORS  Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE    Full-length cDNA libraries and normalization
JOURNAL  Unpublished (2001)
COMMENT  Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 11066.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1077CA09QPl&cluster=11066.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1077CA09QPl.

FEATURES
source
1..1015
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1077YB17"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-Gligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 5,11e-167 Length: 1015
Score: 1440.00 Matches: 273
Percent Similarity: 96.62% Conservative: 13
Best Local Similarity: 92.23% Mismatches: 9
Query Match: 93.32% Indels: 1
Dbs: 13 Gaps: 0

US-09-811-094-33 (1-298) x BX360934 (1-1015)

Qy      1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
Db      128 ATGACAGATGCGGCTGTCTCTTCCCAAGGACATCTCTGGCAGGTGGAGTGGCGCGCAGCC 187
Qy      21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db      188 ATCTCCAGACGGCGGTAGCCCATGACGGCGGTCAAGCTGCTGCTGCGAGGTGCAGCAT 247
Qy      41 AlaSerLysGlnIleAlaAlaAspLysGlnTrpLysGlyIleValAspCysIleValArg 60
Db      248 GCCAGCAGCAGATCACTGCGAGATAAGCAATACAAAGGCATTATAGACTGGGTGCTCGT 307
Qy      61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaValIleArg 80
Db      308 ATTCCTCAAGGAGCGGGAGTCTGTCTCTTGTGGCGGTAACTGACCTGGGCAATGTCTCAGA 367

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Qy      81 TyrPheProThrGlnAlaLeuAenPheAlaPheLysAspLysTrpLysGlnIlePheLeu 100
Db      368 TACTTCCCCACCCAGGCTCTTACTTTCGCTTCAAAGATAAATAACAAGCAGATCTTCTCTG 427
Qy      101 GlyGlyValAspLysHisThrGlnPheTrpArgTrpPheAlaGlyAsnLeuAlaSerGly 120
Db      428 GGTGGGTGGTGGACAGAGAACCCAGATTTTGGCGCTACTTTTCAGAGGAATCTGGCATCGGT 487
Qy      121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTrpProLeuAspPheAlaArgThrArg 140
Db      488 GGTGCCGCGAGGGGCCACATCCCTGTGTTTTGTGTACCTCTTGTATTTTCCCGTACCCGT 547
Qy      141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db      548 CTAGCAGCTGATGGGTAAAGCTGGAGCTGAAAGGGAATTCGAGGCCCTCGGTGACTGC 607
Qy      161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTrpGlnGlyPheSerValSer 180
Db      608 CTGGTTAAGATCTACAAATCTGATGGATTAAAGGCTGTACCAAGGCTTTAAGCTGTCT 667
Qy      181 ValGlnGlyIleIleIleTrpArgAlaAlaTrpPheGlyValTrpAspThrAlaLysGly 200
Db      668 GTCCAGGGTATTATCATCTACCGAGCGCTACTTTCGGTATCTATGACACTGCAAGGGA 727
Qy      201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db      728 ATGCTTCCGATCCCAAGAACACTCATCTGTCATCAGCTGGATGATGCCACAGACTGTC 787
Qy      221 ThrAlaValAlaGlyValValSerTrpProPheAspThrValArgArgMetMetMet 240
Db      788 ACTGCTGTTCGGGGTGTACTTCTTATCCATTGACACCGTTCCGCGCGCATGATGATG 847
Qy      241 GlnSerGlyArgLysGlyAlaAspIleMetTrpGlyThrValAspCysTrpArgLys 260
Db      848 CAGTCAGGCGCAAGGAACTGACATCATGTACAGGCACCGCTGACTGCTGGCGGGAAG 907
Qy      261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyValAlaTrpSerAsnValLeuArg 280
Db      908 ATTGCTCGTGATGAGAGGCAAGAGCTTTTTCAGAGGTGATGTCCTCAATCTTCTCAGA 967
Qy      281 GlyMet-GlyGlyAlaPheValLeuValLeuValLeuValLeuValLeuValLeuLys 295
Db      968 GGCATCGGGTGTGCTTTTGTGCTTCTCTGTATGATGATGATGATGATGATGATGATGAT 1013

RESULT 15
LOCUS   CK024940
DEFINITION CK024940 1064 bp mRNA linear EST 26-NOV-2003
AGENCOURT_16619618 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7049923
5', mRNA sequence.
ACCESSION CK024940
VERSION   CK024940.1 GI:38550864
KEYWORDS EST.
SOURCE   Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 1064)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue procurement: Len Zon, Harvard
cDNA library preparation: Open Biosystems
cDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov
 Plate: LLAM14819 row: p column: 17
 High quality sequence stop: 860.

FEATURES

source

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1. 1064
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   /mol_type="mRNA"
   /db_xref="taxon:7955"
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   /tissue_type="whole body"
   /lab_host="DH10B"
   /clone_lib="NIH ZGC 10"
   /note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A
normalized version of this library is also available
(NIH_ZGC 7). Library was constructed by Open Biosystems
(Huntsville, AL)."
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ORIGIN

Alignment Scores:

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Pred. No.:      9,73e-167      Length:      1064
Score:          1438.00        Matches:      272
Percent Similarity: 96.64%      Conservative: 16
Best Local Similarity: 91.28%    Mismatches:   10
Query Match:     93.20%         Indels:       0
DB:              14            Gaps:         0
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US-09-811-094-33 (1-298) x CK024940 (1-1064)

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Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyLeuAlaAla 20
Db 73 ATGAGTGAGCGGCGCATCTCTTCCCAAGGACTTCTTGGCGGGTGGTATTGGCGGTGCC 132
Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 133 ATCTCTAAACCGCGCGTGGCCCCATTGAGAGAGTCAAACTGCTGCTCAGGTGCACAT 192
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 193 GCTAGCAAAACAGATTACAGCAGATTAAGCAGTACAAAGGCGCATTTATGGACTGGTGGCGT 252
Qy 61 IleProLysGluGlnGlyValLeuSerPheThrPArgGlyAsnLeuAlaAsnValIleArg 80
Db 253 ATCCCCAAGGAGCAGGGCTTCCTGCTGTTCTGGAGAGGAACCTTGGCCCAACGTATACGA 312
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 313 TACTTCCCCACACAGCGCCCTCAACTTTGCTTTCAAGGACAAGTACAGAAGGTCTTCCTT 372
Qy 101 GlyGlyValAspLysHisThrGlnPheThrPArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 373 GATGTGTGGACAAGCGCACCATCCCTCTGCTTGTGTATCCCTTGACTTCGCAAGAACCCGT 432
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 433 GGTGTGTGTGTGGTGCACATCCCTCTGCTTGTGTATCCCTTGACTTCGCAAGAACCCGT 492
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 493 CTTGTGCGCGATGTCGGAAGAGTGGAGCAGAAAGAGAGATTTCAGTGGGCTGGGTAACTGC 552
Qy 161 LeuValIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 553 TTGGTAAAGATCTCAAAATCTGATGGCATCAAGGGTCTGTACCAGGGCTTCAACGTGTCC 612
Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaIleTyrPheGlyValTyrAspThrAlaLysGly 200
Db 613 GTGAGGGTATCATCATTTACAGAGCTGCTACTTCTCGGCATTTATGACACAGCCCAAGGTT 672
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Search completed: August 17, 2004, 20:23:02

Job time : 2952 secs

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Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTyrPheMetIleAlaGlnThrVal 220
Db 673 ATGCTCCCGATCCCAAGAACACCCCATATTGTGTGAGCTGGATGATGCTCAGAGTGTG 732
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 733 ACTGCTGTTGCTGGTCTTCTTCTTACCCCTTCGACACAGTGGTGGTGTATGATGATG 792
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260
Db 793 CAGTCTGGACGTAAGGAGCTGACATCATGTACAGTGGCACAATTCGACTGCTGGAGGAAG 852
Qy 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaThrPheSerAsnValLeuArg 280
Db 853 ATGCGACGTGATGAGGTGGCAAGGCTTTCTTCAAGAGGAGCCCTGGTCAACGTTCTCAGA 912
Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
Db 913 GGCATGGTGGCGCCCTTGTGCTGGTCTTGTATGATGATGAGCTTGAGAAGGTCATT 966
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